

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 29, 2006, 14:01:34 ; Search time 49 Seconds
(without alignments)
464,448 Million cell updates/sec

Title: US-09-502-176-2

Perfect score: 1540

Sequence: 1 VYLSECKTGNGKNGYGTWSK.....TNSQVRWEYCKIPSCDSPPV 260

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1540	100.0	260	2	US-09-982-516-1
2	1535	99.7	339	1	US-08-248-629A-3
3	1535	99.7	339	1	US-08-451-932-3
4	1535	99.7	339	1	US-08-452-260-3
5	1535	99.7	339	1	US-08-326-785-3
6	1535	99.7	339	1	US-08-612-788-3
7	1535	99.7	339	1	US-08-605-598B-3
8	1535	99.7	339	1	US-08-429-743-3
9	1535	99.7	339	1	US-08-866-735-3
10	1535	99.7	339	2	US-09-066-028-3
11	1535	99.7	339	2	US-09-335-325-3
12	1535	99.7	339	2	US-09-335-614-3
13	1535	99.7	339	5	PCT-US95-05107-3
14	1535	99.7	374	2	US-09-377-250-3
15	1535	99.7	375	2	US-09-377-250-2
16	1535	99.7	378	1	US-08-612-788-42
17	1535	99.7	378	2	US-09-066-028-42
18	1535	99.7	378	2	US-09-206-059-1
19	1535	99.7	378	2	US-09-335-325-42
20	1535	99.7	378	2	US-09-335-614-42
21	1535	99.7	451	2	US-09-377-250-1
22	1535	99.7	452	2	US-09-377-250-4
23	1535	99.7	568	3	US-09-946-893C-5
24	1535	99.7	570	3	US-09-946-893C-8
25	1535	99.7	575	3	US-09-946-893C-6
26	1535	99.7	790	1	US-08-469-486-54

ALIGNMENTS

RESULT 1

US-09-982-516-1

; Sequence 1, Application US/09982516

; Patent No. 6723536

; GENERAL INFORMATION:

; APPLICANT: Madsen, John

; APPLICANT: Liang, Hong

; APPLICANT: Sim, Kim Lee

; APPLICANT: Zhou, Xinhua

; APPLICANT: Chang-Murad, Amy

; APPLICANT: Boerner, Renee J.

; APPLICANT: Bermejo, Lourdes L.

; APPLICANT: Mistry, Firoz R.

; APPLICANT: Schrimsher, Jeffrey L.

; APPLICANT: Shepard, Scott R.

; TITLE OF INVENTION: Method of Producing and Purifying Angiotensin Protein

; FILE REFERENCE: 05213-0562 43170-264313

; CURRENT APPLICATION NUMBER: US/09/982,516

; CURRENT FILING DATE: 2002-09-10

; PRIOR APPLICATION NUMBER: PCT/US00/32843

; PRIOR FILING DATE: 2000-12-04

; PRIOR APPLICATION NUMBER: US 60/168,919

; PRIOR FILING DATE: 1999-12-03

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 260

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-982-516-1

Query Match 100.0%; Score 1540; DB 2; Length 260;
Best Local Similarity 100.0%; Pred. No. 3.6e-139;
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	VYLSECKTGNGKNGYGTWSKNGITCKQWSSTSPHRPSPATHPSEGLEENYCRNPDN	60
DB	1	VYLSECKTGNGKNGYGTWSKNGITCKQWSSTSPHRPSPATHPSEGLEENYCRNPDN	60
QY	61	DPQGPWCYTTDEKRYDYCDILECEECNHCSENGYDGIKSKTMSGLEQAWDSQSPHAH	120
DB	61	DPQGPWCYTTDEKRYDYCDILECEECNHCSENGYDGIKSKTMSGLEQAWDSQSPHAH	120
QY	121	GYIPSKFPNKLKQNYCRNPDRPWCFTTDPNKRWELCDIPRCTTPPPSGGTYQCLK	180
DB	121	GYIPSKFPNKLKQNYCRNPDRPWCFTTDPNKRWELCDIPRCTTPPPSGGTYQCLK	180
QY	181	GTGNYRGVATVSGHTCOHWSAQTPHHTPFPCKNLNDENYCRPDGGRAPWCHT	240

Db 181 GTGENYRGNVAVTVSGHTCQHWSAQTPHTHTERTPENFPCKNLNDENYCRNPDGKRAPWCHT 240

Qy 241 TNSQVRWEYCKIPSCDSSPV 260
Db 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 2

US-08-248-629A-3
; Sequence 3, Application US/08248629A
; Patent No. 5639725
; GENERAL INFORMATION:
; APPLICANT: Folkman, Judah
; APPLICANT: O'Reilly, Michael
; TITLE OF INVENTION: Angiostatin and Method of Use
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jones & Askew
; STREET: 191 Peachtree Street, 37th Floor
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303-1769

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50
; COMPUTER: Macintosh
; OPERATING SYSTEM: 7.0
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/248,629A
; FILING DATE: 04/26/94
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Larry W. Stults, Ph.D.
; REGISTRATION NUMBER: 34,025
; REFERENCE/DOCKET NUMBER: 05213-0120
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-818-3700
; TELEFAX: 404-818-3799
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339
; TYPE: amino acid
; TOPOLOGY: linear
US-08-248-629A-3

Query Match 99.7%; Score 1535; DB 1; Length 339;
Best Local Similarity 99.6%; Pred. No. 1.5e-138;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VYLSECKTGNGKNYRGTMSKTKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN 60

Db 1 VYLSECKTGNGKNYRGTMSKTKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN 60

Qy 61 DPQGPWCYTTDPKRYDYCDIILECEBECMHCSGENTDGIKSKTMSGLECQAWDSQSPHAA 120

Db 61 DPQGPWCYTTDPKRYDYCDIILECEBECMHCSGENTDGIKSKTMSGLECQAWDSQSPHAA 120

Qy 121 GYIPSKFPNNLKNKYNCRNPDRELPCWCTTDPNKKWELCDIPRCTTTPPSSGPTYOCLK 180

Db 121 GYIPSKFPNNLKNKYNCRNPDRELPCWCTTDPNKKWELCDIPRCTTTPPSSGPTYOCLK 180

Qy 181 GTGENYRGNVAVTVSGHTCQHWSAQTPHTHTERTPENFPCKNLNDENYCRNPDGKRAPWCHT 240

Db 181 GTGENYRGNVAVTVSGHTCQHWSAQTPHTHTERTPENFPCKNLNDENYCRNPDGKRAPWCHT 240

Qy 241 TNSQVRWEYCKIPSCDSSPV 260
Db 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 3

US-08-451-932-3
; Sequence 3, Application US/08451932
; Patent No. 5733876
; GENERAL INFORMATION:
; APPLICANT: Folkman, Judah
; APPLICANT: O'Reilly, Michael
; TITLE OF INVENTION: Method of Treating an Angiogenic
; TITLE OF INVENTION: Disease
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jones & Askew
; STREET: 191 Peachtree Street, 37th Floor
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303-1769

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50
; COMPUTER: Macintosh
; OPERATING SYSTEM: 7.0
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/451,932
; FILING DATE: 05/26/95
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/248,629
; FILING DATE: 04/26/94
; ATTORNEY/AGENT INFORMATION:
; NAME: Larry W. Stults, Ph.D.
; REGISTRATION NUMBER: 34,025
; REFERENCE/DOCKET NUMBER: 05213-0123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-818-3700
; TELEFAX: 404-818-3799
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339
; TYPE: amino acid
; TOPOLOGY: linear
US-08-451-932-3

Query Match 99.7%; Score 1535; DB 1; Length 339;
Best Local Similarity 99.6%; Pred. No. 1.5e-138;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VYLSECKTGNGKNYRGTMSKTKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN 60

Db 1 VYLSECKTGNGKNYRGTMSKTKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN 60

Qy 61 DPQGPWCYTTDPKRYDYCDIILECEBECMHCSGENTDGIKSKTMSGLECQAWDSQSPHAA 120

Db 61 DPQGPWCYTTDPKRYDYCDIILECEBECMHCSGENTDGIKSKTMSGLECQAWDSQSPHAA 120

Qy 121 GYIPSKFPNNLKNKYNCRNPDRELPCWCTTDPNKKWELCDIPRCTTTPPSSGPTYOCLK 180

Db 121 GYIPSKFPNNLKNKYNCRNPDRELPCWCTTDPNKKWELCDIPRCTTTPPSSGPTYOCLK 180

Qy 181 GTGENYRGNVAVTVSGHTCQHWSAQTPHTHTERTPENFPCKNLNDENYCRNPDGKRAPWCHT 240

Db 181 GTGENYRGNVAVTVSGHTCQHWSAQTPHTHTERTPENFPCKNLNDENYCRNPDGKRAPWCHT 240

Qy 241 TNSQVRWEYCKIPSCDSSPV 260
Db 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 4

US-08-452-260-3
; Sequence 3, Application US/08452260
; Patent No. 5776704

GENERAL INFORMATION:
APPLICANT: Folkman, Judah
APPLICANT: O'Reilly, Michael
TITLE OF INVENTION: Method of Diagnosing an Angiogenic
Disease
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50
COMPUTER: Macintosh
OPERATING SYSTEM: 7.0
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/452,260
FILING DATE: 05/26/95
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/248,629
FILING DATE: 04/26/94
ATTORNEY/AGENT INFORMATION:
NAME: Larry W. Stults, Ph.D.
REGISTRATION NUMBER: 34,025
REFERENCE/DOCKET NUMBER: 05213-0124
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 339
TYPE: amino acid
TOPOLOGY: linear
US-08-452-260-3

Query Match 99.7%; Score 1535; DB 1; Length 339;
Best Local Similarity 99.6%; Pred. No. 1.5e-138;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGYGTMSKNGITCKQWSSTSPHRPSPATHPSEGLEENYCRNPDN 60
DB 1 VYLSECKTGNGKNGYGTMSKNGITCKQWSSTSPHRPSPATHPSEGLEENYCRNPDN 60
QY 61 DPQGPWCYTTDPKRYDYCDILLECEBECMHCSENGYDGKISKTMSGLECOQWDSQSPH 120
DB 61 DPQGPWCYTTDPKRYDYCDILLECEBECMHCSENGYDGKISKTMSGLECOQWDSQSPH 120
QY 121 GYIPSKFPNKLKQNYCRNPDRELPCWCTTDPNKEWELCDIPRCTTTPPSSGPTYQCLK 180
DB 121 GYIPSKFPNKLKQNYCRNPDRELPCWCTTDPNKEWELCDIPRCTTTPPSSGPTYQCLK 180
QY 181 GTGENTRGNAVTVSGHTCOHWSAQTPHTHTPTNPFCNLDENYCRNPDGKRAPWCHT 240
DB 181 GTGENTRGNAVTVSGHTCOHWSAQTPHTHTPTNPFCNLDENYCRNPDGKRAPWCHT 240
QY 241 TNSQVRWEYCKIPSCDSSPV 260
DB 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 5
US-08-326-785-3
Sequence 3, Application US/08326785
Patent No. 5792845
GENERAL INFORMATION:
APPLICANT: Folkman, Judah
APPLICANT: O'Reilly, Michael
TITLE OF INVENTION: Angiostatin and Method of Use
NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50
COMPUTER: Macintosh
OPERATING SYSTEM: 7.0
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/326,785
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/248,629
FILING DATE: 04/26/94
ATTORNEY/AGENT INFORMATION:
NAME: Larry W. Stults, Ph.D.
REGISTRATION NUMBER: 34,025
REFERENCE/DOCKET NUMBER: 05213-0121
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 339
TYPE: amino acid
TOPOLOGY: linear
US-08-326-785-3

Query Match 99.7%; Score 1535; DB 1; Length 339;
Best Local Similarity 99.6%; Pred. No. 1.5e-138;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGYGTMSKNGITCKQWSSTSPHRPSPATHPSEGLEENYCRNPDN 60
DB 1 VYLSECKTGNGKNGYGTMSKNGITCKQWSSTSPHRPSPATHPSEGLEENYCRNPDN 60
QY 61 DPQGPWCYTTDPKRYDYCDILLECEBECMHCSENGYDGKISKTMSGLECOQWDSQSPH 120
DB 61 DPQGPWCYTTDPKRYDYCDILLECEBECMHCSENGYDGKISKTMSGLECOQWDSQSPH 120
QY 121 GYIPSKFPNKLKQNYCRNPDRELPCWCTTDPNKEWELCDIPRCTTTPPSSGPTYQCLK 180
DB 121 GYIPSKFPNKLKQNYCRNPDRELPCWCTTDPNKEWELCDIPRCTTTPPSSGPTYQCLK 180
QY 181 GTGENTRGNAVTVSGHTCOHWSAQTPHTHTPTNPFCNLDENYCRNPDGKRAPWCHT 240
DB 181 GTGENTRGNAVTVSGHTCOHWSAQTPHTHTPTNPFCNLDENYCRNPDGKRAPWCHT 240
QY 241 TNSQVRWEYCKIPSCDSSPV 260
DB 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 6
US-08-612-788-3
Sequence 3, Application US/08612788
Patent No. 5837682
GENERAL INFORMATION:
APPLICANT: Folkman, M. Judah
APPLICANT: O'Reilly, Micheal
APPLICANT: Cao, Yihai
APPLICANT: Sim, B. Kim Lee
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta

STATE: Georgia
COUNTRY: U.S.
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,788
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05213-0126
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: Angiostatin fragment
US-08-612-788-3

Query Match 99.7%; Score 1535; DB 1; Length 339;
Best Local Similarity 99.6%; Pred. No. 1.5e-138;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGYRTGMSKNGITCQKWSSTSPHRPFSATHPSEGLEENYCRNPON 60
DB 1 VYLSECKTGNGKNGYRTGMSKNGITCQKWSSTSPHRPFSATHPSEGLEENYCRNPON 60

QY 61 DPQGPWCYTTDEPKRYDYCDILECEECMHCSENGYDGIKSKTMSGLECQAWDSQSPH 120
DB 61 DPQGPWCYTTDEPKRYDYCDILECEECMHCSENGYDGIKSKTMSGLECQAWDSQSPH 120

QY 121 GIYPSKFPNKLKNGYCRNPDRRLPWCFTTDPNKRWELCDIPRCTTTPSSGPTYQCLK 180
DB 121 GIYPSKFPNKLKNGYCRNPDRRLPWCFTTDPNKRWELCDIPRCTTTPSSGPTYQCLK 180

QY 181 GTGENYRGNVAVTVSGHTCOHWSAQTPHTHTERTPENFCKNLNDENYCRNPDKGRAPWCHT 240
DB 181 GTGENYRGNVAVTVSGHTCOHWSAQTPHTHTERTPENFCKNLNDENYCRNPDKGRAPWCHT 240

QY 241 TNSQVRWEYCKIPSCDSSPV 260
DB 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 7
US-08-605-598B-3
Sequence 3, Application US/08605598B
Patent No. 5861372
GENERAL INFORMATION:
APPLICANT: Folkman, M. Judah
APPLICANT: Lin, Jie
APPLICANT: O'Reilly, Michael S.
TITLE OF INVENTION: Aggregate Angiostatin and Method of Use
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor

CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,598B
FILING DATE: 22-FEB-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05213-0127
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Human Angiostatin
US-08-605-598B-3

Query Match 99.7%; Score 1535; DB 1; Length 339;
Best Local Similarity 99.6%; Pred. No. 1.5e-138;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGYRTGMSKNGITCQKWSSTSPHRPFSATHPSEGLEENYCRNPON 60
DB 1 VYLSECKTGNGKNGYRTGMSKNGITCQKWSSTSPHRPFSATHPSEGLEENYCRNPON 60

QY 61 DPQGPWCYTTDEPKRYDYCDILECEECMHCSENGYDGIKSKTMSGLECQAWDSQSPH 120
DB 61 DPQGPWCYTTDEPKRYDYCDILECEECMHCSENGYDGIKSKTMSGLECQAWDSQSPH 120

QY 121 GIYPSKFPNKLKNGYCRNPDRRLPWCFTTDPNKRWELCDIPRCTTTPSSGPTYQCLK 180
DB 121 GIYPSKFPNKLKNGYCRNPDRRLPWCFTTDPNKRWELCDIPRCTTTPSSGPTYQCLK 180

QY 181 GTGENYRGNVAVTVSGHTCOHWSAQTPHTHTERTPENFCKNLNDENYCRNPDKGRAPWCHT 240
DB 181 GTGENYRGNVAVTVSGHTCOHWSAQTPHTHTERTPENFCKNLNDENYCRNPDKGRAPWCHT 240

QY 241 TNSQVRWEYCKIPSCDSSPV 260
DB 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 8
US-08-429-743-3
Sequence 3, Application US/08429743
Patent No. 5885795
GENERAL INFORMATION:
APPLICANT: O'Reilly, Michael
APPLICANT: Folkman, M. Judah
APPLICANT: Sim, Kim Lee
APPLICANT: Cao, Yihai
TITLE OF INVENTION: Angiostatin and Method of Use
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.

STATE: Georgia
COUNTRY: USA
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/429,743
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,629
FILING DATE: 26-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/326,785
FILING DATE: 20-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Johnson, James D.
REGISTRATION NUMBER: 31,771
REFERENCE/DOCKET NUMBER: 05213-0122
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CLONE: Angiotatin fragment
US-08-429-743-3

Query Match 99.7%; Score 1535; DB 1; Length 339;
Best Local Similarity 99.6%; Pred. No. 1.5e-138;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGNYRTGMSKTKNGITCQKWSSTSPHRPSPATHPSGLSENYCRNPDN 60
DB 1 VYLSECKTGNGNYRTGMSKTKNGITCQKWSSTSPHRPSPATHPSGLSENYCRNPDN 60

QY 61 DPQGPWCYTTPDEKRYDYCDILECEECMHCSENYDGIKSKTMSGLEQAWDSQSPH 120
DB 61 DPQGPWCYTTPDEKRYDYCDILECEECMHCSENYDGIKSKTMSGLEQAWDSQSPH 120

QY 121 GYIPSPFNKLNKXNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTTPSSGPTYQCLK 180
DB 121 GYIPSPFNKLNKXNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTTPSSGPTYQCLK 180

QY 181 GTGENYRGNAVTVSGHTCQHSQAOTPHHTERTPENFPCKNLNDENYCRNPDGKRAPWCHT 240
DB 181 GTGENYRGNAVTVSGHTCQHSQAOTPHHTERTPENFPCKNLNDENYCRNPDGKRAPWCHT 240

QY 241 TNSQVRWEYCKIPSCDSSPV 260
DB 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 9
US-08-866-735-3
Sequence 3, Application US/08866735
Patent No. 5945403
GENERAL INFORMATION:
APPLICANT: Folkman, M. Judah
APPLICANT: O'Reilly, Michael
TITLE OF INVENTION: Angiotatin Fragments and Method of Use
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew, LLP
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta

STATE: Georgia
COUNTRY: USA
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/866,735
FILING DATE: 30-MAY-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05940-0129
TELEPHONE: (404) 818-3700
TELEFAX: (404) 818-3799
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: Angiotatin fragment
US-08-866-735-3

Query Match 99.7%; Score 1535; DB 1; Length 339;
Best Local Similarity 99.6%; Pred. No. 1.5e-138;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGNYRTGMSKTKNGITCQKWSSTSPHRPSPATHPSGLSENYCRNPDN 60
DB 1 VYLSECKTGNGNYRTGMSKTKNGITCQKWSSTSPHRPSPATHPSGLSENYCRNPDN 60

QY 61 DPQGPWCYTTPDEKRYDYCDILECEECMHCSENYDGIKSKTMSGLEQAWDSQSPH 120
DB 61 DPQGPWCYTTPDEKRYDYCDILECEECMHCSENYDGIKSKTMSGLEQAWDSQSPH 120

QY 121 GYIPSPFNKLNKXNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTTPSSGPTYQCLK 180
DB 121 GYIPSPFNKLNKXNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTTPSSGPTYQCLK 180

QY 181 GTGENYRGNAVTVSGHTCQHSQAOTPHHTERTPENFPCKNLNDENYCRNPDGKRAPWCHT 240
DB 181 GTGENYRGNAVTVSGHTCQHSQAOTPHHTERTPENFPCKNLNDENYCRNPDGKRAPWCHT 240

QY 241 TNSQVRWEYCKIPSCDSSPV 260
DB 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 10
US-09-066-028-3
Sequence 3, Application US/09066028
Patent No. 6024688
GENERAL INFORMATION:
APPLICANT: Folkman, M. Judah
APPLICANT: O'Reilly, Michael
TITLE OF INVENTION: Angiotatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew

STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: US/09/066,028
APPLICATION NUMBER: 08/612,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05213-0126
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: Angiostatin fragment
US-09-066-028-3

Query Match 99.7%; Score 1535; DB 2; Length 339;
Best Local Similarity 99.6%; Pred. No. 1.5e-138;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 VYLSECKTGNGKNGYRGTMSTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN 60
DB 1 VYLSECKTGNGKNGYRGTMSTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN 60
QY 61 DPQGPWCYTTDPKRYDYCDILECEECHCSENYDGIKSKTMSGLECOQWDSQSPHAAH 120
DB 61 DPQGPWCYTTDPKRYDYCDILECEECHCSENYDGIKSKTMSGLECOQWDSQSPHAAH 120
QY 121 GYIPSKFPNKLKKNYCRNPDRELPCWCTTDPNKRWELCDIPRCTTTPPPSSGPTYQCCLK 180
DB 121 GYIPSKFPNKLKKNYCRNPDRELPCWCTTDPNKRWELCDIPRCTTTPPPSSGPTYQCCLK 180
QY 181 GTGENYRGNAVTVSGHTCOHWSAQTPHTHTPTENFPCKNLDENYCRNPDGKRAPWCHT 240
DB 181 GTGENYRGNAVTVSGHTCOHWSAQTPHTHTPTENFPCKNLDENYCRNPDGKRAPWCHT 240
QY 241 TNSQVRWEYCKIPSCDSSPV 260
DB 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 11
US-09-335-325-3
Sequence 3, Application US/09335325
Patent No. 6521439
GENERAL INFORMATION:
APPLICANT: Folkman, M. Judah
O'Reilly, Micheal
Cao, Yihai

Sim, B. Kim Lee
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/335,325
FILING DATE: 17-Jun-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/612,788
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05213-0126
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: Angiostatin fragment
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-335-325-3
Query Match 99.7%; Score 1535; DB 2; Length 339;
Best Local Similarity 99.6%; Pred. No. 1.5e-138;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 VYLSECKTGNGKNGYRGTMSTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN 60
DB 1 VYLSECKTGNGKNGYRGTMSTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN 60
QY 61 DPQGPWCYTTDPKRYDYCDILECEECHCSENYDGIKSKTMSGLECOQWDSQSPHAAH 120
DB 61 DPQGPWCYTTDPKRYDYCDILECEECHCSENYDGIKSKTMSGLECOQWDSQSPHAAH 120
QY 121 GYIPSKFPNKLKKNYCRNPDRELPCWCTTDPNKRWELCDIPRCTTTPPPSSGPTYQCCLK 180
DB 121 GYIPSKFPNKLKKNYCRNPDRELPCWCTTDPNKRWELCDIPRCTTTPPPSSGPTYQCCLK 180
QY 181 GTGENYRGNAVTVSGHTCOHWSAQTPHTHTPTENFPCKNLDENYCRNPDGKRAPWCHT 240
DB 181 GTGENYRGNAVTVSGHTCOHWSAQTPHTHTPTENFPCKNLDENYCRNPDGKRAPWCHT 240
QY 241 TNSQVRWEYCKIPSCDSSPV 260
DB 241 TNSQVRWEYCKIPSCDSSPV 260
RESULT 12
US-09-335-614-3

Sequence 3, Application US/09335614
Patent No. 6949511
GENERAL INFORMATION:
APPLICANT: Folkman, M. Judah
O'Reilly, Micheal
Cao, Yihai
Sim, B. Kim Lee
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/335,614
FILING DATE: 18-Jun-1999
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/612,788
FILING DATE: 08-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05213-0126
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: Angiostatin fragment
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-335-614-3

Query Match 99.7%; Score 1535; DB 2; Length 339;
Best Local Similarity 99.6%; Pred. No. 1.5e-138;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 VYLSECKTGNGNYRGTMSTKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN 60
DB 1 VYLSECKTGNGNYRGTMSTKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN 60
QY 61 DPQGPWCYTTDEPKRYDYCDIILECEBECMHCSENGYDGIKSKTMSGLECOQWDSQSPH 120
DB 61 DPQGPWCYTTDEPKRYDYCDIILECEBECMHCSENGYDGIKSKTMSGLECOQWDSQSPH 120
QY 121 GYIPKFPNKLKKNYCRNPDRELPCWCTTDPNKRWELCDIPRCTTTPPSSGPTYQCLK 180
DB 121 GYIPKFPNKLKKNYCRNPDRELPCWCTTDPNKRWELCDIPRCTTTPPSSGPTYQCLK 180
QY 181 GTGNYRGNAVTVSGHTCQHWSAQTPHTHTPTNPFCNLDENYCRNPDGKRAPWCHT 240
DB 181 GTGNYRGNAVTVSGHTCQHWSAQTPHTHTNPFCNLDENYCRNPDGKRAPWCHT 240
QY 241 TNSQVRWEYCKIPSCDSSPV 260

Db 241 TNSQVRWEYCKIPSCDSSPV 260
RESULT 13
PCT-US95-05107-3
Sequence 3, Application PC/TUS9505107
GENERAL INFORMATION:
APPLICANT: THE CHILDREN'S MEDICAL CENTER, CORPORATION
TITLE OF INVENTION: Angiostatin and Method of Use
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05107
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,629
FILING DATE: 26-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/326,785
FILING DATE: 20-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Johnson, James D.
REGISTRATION NUMBER: 31,771
REFERENCE/DOCKET NUMBER: 05213-0122
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
PCT-US95-05107-3

Query Match 99.7%; Score 1535; DB 5; Length 339;
Best Local Similarity 99.6%; Pred. No. 1.5e-138;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 VYLSECKTGNGNYRGTMSTKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN 60
DB 1 VYLSECKTGNGNYRGTMSTKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN 60
QY 61 DPQGPWCYTTDEPKRYDYCDIILECEBECMHCSENGYDGIKSKTMSGLECOQWDSQSPH 120
DB 61 DPQGPWCYTTDEPKRYDYCDIILECEBECMHCSENGYDGIKSKTMSGLECOQWDSQSPH 120
QY 121 GYIPKFPNKLKKNYCRNPDRELPCWCTTDPNKRWELCDIPRCTTTPPSSGPTYQCLK 180
DB 121 GYIPKFPNKLKKNYCRNPDRELPCWCTTDPNKRWELCDIPRCTTTPPSSGPTYQCLK 180
QY 181 GTGNYRGNAVTVSGHTCQHWSAQTPHTHTPTNPFCNLDENYCRNPDGKRAPWCHT 240
DB 181 GTGNYRGNAVTVSGHTCQHWSAQTPHTHTNPFCNLDENYCRNPDGKRAPWCHT 240
QY 241 TNSQVRWEYCKIPSCDSSPV 260

Db 241 TNSQVRWEYCKIPSCDSSPV 260
|||||

RESULT 14
US-09-377-250-3
; Sequence 3, Application US/09377250
; Patent No. 6365364
; GENERAL INFORMATION:
; APPLICANT: MANN, KENNETH G.
; APPLICANT: SWORDS JENNY, NANCY
; TITLE OF INVENTION: ANGIOGENESIS INHIBITORS AND USERS THEREOF
; FILE REFERENCE: 48409/360
; CURRENT APPLICATION NUMBER: US/09/377,250
; CURRENT FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: angiogenesis inhibitor
; NAME/KEY: MOD RES
; LOCATION: (264)
; OTHER INFORMATION: Xaa = Gln or Glu
US-09-377-250-3

Query Match 99.7%; Score 1535; DB 2; Length 374;
Best Local Similarity 99.6%; Pred. No. 1.7e-138;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 VYLSECKTGNGKNGYRGTMKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN 60
Db 1 VYLSECKTGNGKNGYRGTMKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN 60
QY 61 DPGGPMCYTTDPKRYDYCDIILECEBECMHCSENGYDGIKSKTMSGLECOAWDSQSPHAH 120
Db 61 DPGGPMCYTTDPKRYDYCDIILECEBECMHCSENGYDGIKSKTMSGLECOAWDSQSPHAH 120
QY 121 GYIPSKFPNKLKKNYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTTPPPSSGPTYQCLK 180
Db 121 GYIPSKFPNKLKKNYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTTPPPSSGPTYQCLK 180
QY 181 GTGENYRGNVAVTVSGHTCQHSQAQTPHTHRTPENFPCKNLDENYCRNPDGKRAPWCHT 240
Db 181 GTGENYRGNVAVTVSGHTCQHSQAQTPHTHRTPENFPCKNLDENYCRNPDGKRAPWCHT 240
QY 241 TNSQVRWEYCKIPSCDSSPV 260
Db 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 15
US-09-377-250-2
; Sequence 2, Application US/09377250
; Patent No. 6365364
; GENERAL INFORMATION:
; APPLICANT: MANN, KENNETH G.
; APPLICANT: SWORDS JENNY, NANCY
; TITLE OF INVENTION: ANGIOGENESIS INHIBITORS AND USERS THEREOF
; FILE REFERENCE: 48409/360
; CURRENT APPLICATION NUMBER: US/09/377,250
; CURRENT FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: angiogenesis inhibitor

; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (265)
; OTHER INFORMATION: Xaa = Gln or Glu
US-09-377-250-2
Query Match 99.7%; Score 1535; DB 2; Length 375;
Best Local Similarity 99.6%; Pred. No. 1.7e-138;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 VYLSECKTGNGKNGYRGTMKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN 60
Db 2 VYLSECKTGNGKNGYRGTMKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN 61
QY 61 DPGGPMCYTTDPKRYDYCDIILECEBECMHCSENGYDGIKSKTMSGLECOAWDSQSPHAH 120
Db 62 DPGGPMCYTTDPKRYDYCDIILECEBECMHCSENGYDGIKSKTMSGLECOAWDSQSPHAH 121
QY 121 GYIPSKFPNKLKKNYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTTPPPSSGPTYQCLK 180
Db 122 GYIPSKFPNKLKKNYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTTPPPSSGPTYQCLK 181
QY 181 GTGENYRGNVAVTVSGHTCQHSQAQTPHTHRTPENFPCKNLDENYCRNPDGKRAPWCHT 240
Db 182 GTGENYRGNVAVTVSGHTCQHSQAQTPHTHRTPENFPCKNLDENYCRNPDGKRAPWCHT 241
QY 241 TNSQVRWEYCKIPSCDSSPV 260
Db 242 TNSQVRWEYCKIPSCDSSPV 261

Search completed: August 29, 2006, 14:02:54
Job time : 50 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 29, 2006, 13:53:08 ; Search time 299 Seconds
(without alignments)
804.361 Million cell updates/sec

Title: US-09-502-176-2

Perfect score: 1540

Sequence: 1 VTLSECKTGNGKNGYRGWTSK.....TNSQVRWEYCKIPSCDSPPV 260

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1535	99.7	810	1	PLMN HUMAN
2	1535	99.7	810	2	Q5TEH4 HUMAN
3	1458	94.7	810	2	Q5R8X6 PONGO PYGMA
4	1442	93.6	810	1	PLMN MACMU
5	1306	84.8	359	2	Q8WNR1 CANIS FAMIL
6	1299	84.4	812	1	PLMN RAT
7	1299	84.4	812	2	Q5BKX6 RAT
8	1292	83.9	790	1	PLMN FIG
9	1291	83.8	812	1	PLMN BOVIN
10	1279	83.1	466	2	Q6TCI0 MOUSE
11	1279	83.1	812	1	PLMN MOUSE
12	1279	83.1	812	2	Q3VLT9 MOUSE
13	1237	80.3	810	1	PLMN ERIEU
14	1203.5	78.1	759	2	Q7TP84 RAT
15	1160	75.3	806	1	PLMN MACCEU
16	996	64.7	818	2	Q6PBA6 BRARE
17	962	62.5	797	2	Q5OLG6 ORVLA
18	959	62.3	814	2	Q5DVP8 ONCMY
19	881	57.2	2869	2	Q28398 ERIEU
20	809.5	52.6	449	2	Q6GP14 XENLA
21	809.5	52.6	716	2	Q91691 XENLA
22	797	51.8	728	1	HGF HUMAN
23	796	51.7	709	2	Q7VTN9 XENLA
24	795.5	51.7	717	2	P70006 XENLA
25	782	50.8	728	1	HGF RAT
26	778	50.5	726	2	Q90978 CHICK
27	777	50.5	730	2	Q867B7 CANFA
28	777	50.5	728	2	Q8C9G5 MOUSE
29	776.5	50.4	710	2	Q91402 9PIPI
30	776	50.4	728	1	HGF MOUSE
31	776	50.4	728	2	Q53WS5 MOUSE

32	774	50.3	730	2	Q76BS1 BOVIN
33	772	50.1	704	2	Q90865 CHICK
34	772	50.1	728	2	Q9BH09 FELCA
35	766.5	49.8	699	2	Q5RGG3 BRARE
36	766.5	49.8	709	2	Q5XFY1 BRARE
37	766.5	49.8	709	2	Q90ZN6 BRARE
38	766.5	49.8	716	2	P70521 RAT
39	758	49.2	655	2	Q4RX92 TETNG
40	756.5	49.1	716	2	Q3UZ05 MOUSE
41	754.5	49.0	405	2	Q788Q2 CHICK
42	753.5	48.9	716	1	HGFL MOUSE
43	753.5	48.9	716	2	Q6GTL1 MOUSE
44	753.5	48.9	716	2	Q91XG8 MOUSE
45	752	48.8	667	2	Q4SUG4 TETNG

ALIGNMENTS

RESULT 1
PLMN_HUMAN STANDARD; PRT; 810 AA.
AC P00747; Q15146; Q6PA00;
DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
DT 01-JUL-1989, sequence version 2.
DT 07-MAR-2006, entry version 92.
DE Plasminogen precursor (EC 3.4.21.7) [Contains: Plasmin heavy chain A;
DE Activation peptide; Angiostatin; Plasmin heavy chain A, short form;
DE Plasmin light chain B].
GN Name=PLG;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE, AND VARIANT ASN-472.
RX MEDLINE=90202879; PubMed=2318848;
RA Petersen T.E., Martzen M.R., Ichinose A., Davie E.W.;
RT "Characterization of the gene for human plasminogen, a key proenzyme
RT in the fibrinolytic system."
RL J. Biol. Chem. 265:6104-6111(1990).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=87162490; PubMed=3030813; DOI=10.1016/0014-5793(87)81501-6;
RA Forsgren M., Raden B., Israelsson M., Larsson K., Heden L.-O.;
RT "Molecular cloning and characterization of a full-length cDNA clone
RT for human plasminogen."
RL FEBS Lett. 213:254-260(1987).
RN [3]
RP NUCLEOTIDE SEQUENCE.
TX TISSUE=Liver;
RA Browne M.J., Chapman C.G., Dodd I., Carey J.E., Lawrence G.M.P.,
RA Mitchell D., Robinson J.H.;
RT "Expression of recombinant human plasminogen and aglycoplasminogen in
RT HeLa cells."
RL Submitted (OCT-1991) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS LYS-57; GLN-133;
RP HIS-261; TRP-408; ASN-472; VAL-494 AND TRP-523.
RA Rieder M.J., Armel T.Z., Carrington D.P., Ozuna M., Kuldane S.A.,
RA Rajkumar N., Toth E.J., Yi Q., Nickerson D.A.;
RT "SeattleSNP: NHLBI HL6682 program for genomic applications, UW-
RT FHCR, Seattle, WA (URL: http://pga.gs.washington.edu).";
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
RN [5]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
TX TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wang J., Hsieh F.,

- RA Piatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonadio M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smillius D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RL and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [16]
 RP PROTEIN SEQUENCE OF 20-810, AND VARIANT ASN-472.
 RA Sotttrup-Jensen L., Petersen T.E., Magnusson S.;
 RL Submitted (JUL-1977) to the PIR data bank.
 RN [17]
 RP NUCLEOTIDE SEQUENCE OF 292-810.
 RX MEDLINE=85023311; PubMed=6148961;
 RA Malinowski D.P., Sadler J.E., Davie E.W.;
 RT "Characterization of a complementary deoxyribonucleic acid coding for
 RT human and bovine plasminogen.";
 RL Biochemistry 23:4243-4250(1984).
 RN [18]
 RP PROTEIN SEQUENCE OF 20-100.
 RX MEDLINE=75093329; PubMed=122932;
 RA Wiman B., Wallen P.;
 RT "Structural relationship between 'glutamic acid' and 'lysine' forms of
 RT human plasminogen and their interaction with the NH2-terminal
 RT activation peptide as studied by affinity chromatography.";
 RL Eur. J. Biochem. 50:489-494(1975).
 RN [19]
 RP PROTEIN SEQUENCE OF 95-580; 581-626; 657-700 AND 732-810, AND VARIANT
 RP ASN-472.
 RA Sotttrup-Jensen L., Claeys H., Zajdel M., Petersen T.E., Magnusson S.;
 RT "The primary structure of human plasminogen.";
 RL (in) Davidson J.F., Rowan R.M., Samama M.M., Desnoyers P.C. (eds.);
 RL Progress in chemical fibrinolysis and thrombolysis, pp.3:191-209,
 RL Raven Press, New York (1978).
 RN [10]
 RP PROTEIN SEQUENCE OF 483-604.
 RX MEDLINE=76043692; PubMed=126863;
 RA Wiman B., Wallen P.;
 RT "Amino-acid sequence of the cyanogen-bromide fragment from human
 RT plasminogen that forms the linkage between the plasmin chains.";
 RL Eur. J. Biochem. 58:539-547(1975).
 RN [11]
 RP PROTEIN SEQUENCE OF 581-810.
 RX MEDLINE=77225245; PubMed=142009;
 RA Wiman B.;
 RT "Primary structure of the B-chain of human plasmin.";
 RL Eur. J. Biochem. 76:129-137(1977).
 RN [12]
 RP ACTIVE SITE.
 RX MEDLINE=73149248; PubMed=4694729;
 RA Robbins K.C., Bernabe P., Arzadon L., Summaria L.;
 RT "The primary structure of human plasminogen. II. The histidine loop of
 RT human plasmin: light (B) chain active center histidine sequence.";
 RL J. Biol. Chem. 248:1631-1633(1973).
 RN [13]
 RP ACTIVE SITE.
 RX MEDLINE=69234739; PubMed=4240117;
 RA Groeskopf W.R., Summaria L., Robbins K.C.;
 RT "Studies on the active center of human plasmin. Partial amino acid
 RT sequence of a peptide containing the active center serine residue.";
 RL J. Biol. Chem. 244:3590-3597(1969).
 RN [14]
 RP OMEGA-AMINOCARBOXYLIC ACID-BINDING SITES.
 RX MEDLINE=82213905; PubMed=6919539;
 RA Trexler M., Vali Z., Patthy L.;
 RT "Structure of the omega-aminocarboxylic acid-binding sites of human
 RT plasminogen. Arginine 70 and aspartic acid 56 are essential for
 RT binding of ligand by kringle 4.";
 RL J. Biol. Chem. 257:7401-7406(1982).
 RN [15]
 RP FIBRIN AND OMEGA-AMINOCARBOXYLIC ACID BINDING SITES.
 RX MEDLINE=85054794; PubMed=6094526;
 RA Vali Z., Patthy L.;
 RT "The fibrin-binding site of human plasminogen. Arginines 32 and 34 are
 RT essential for fibrin affinity of the kringle 1 domain.";
 RL J. Biol. Chem. 259:13690-13694(1984).
 RN [16]
 RP PHOSPHORYLATION SITE SER-597.
 RX MEDLINE=97345939; PubMed=9201958; DOI=10.1021/bi970328d;
 RA Wang H., Prorok M., Bretthauer R.K., Castellino F.J.;
 RT "Serine-578 is a major phosphorylation locus in human plasma
 RT plasminogen.";
 RL Biochemistry 36:8100-8106(1997).
 RN [17]
 RP CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=88185329; PubMed=3356193;
 RA Marti T., Schaller J., Rickli E.E., Schmid K., Kamerling J.P.,
 RA Gerwig G.J., van Halbeek H., Vliegenthart J.F.;
 RT "The N- and O-linked carbohydrate chains of human, bovine and porcine
 RT plasminogen. Species specificity in relation to sialylation and
 RT fucosylation patterns.";
 RL Eur. J. Biochem. 173:57-63(1988).
 RN [18]
 RP CARBOHYDRATE-LINKAGE SITE SER-268.
 RX MEDLINE=97207306; PubMed=9054441; DOI=10.1074/jbc.272.11.7408;
 RA Pirie-Shepherd S.R., Stevens R.D., Andon N.L., Enghild J.J.,
 RA Pizzo S.V.;
 RT "Evidence for a novel O-linked sialylated trisaccharide on Ser-248 of
 RT human plasminogen 2.";
 RL J. Biol. Chem. 272:7408-7411(1997).
 RN [19]
 RP CHARACTERIZATION OF ANGIOTATIN, AND PARTIAL PROTEIN SEQUENCE.
 RX MEDLINE=95042728; PubMed=7525077; DOI=10.1016/0092-8674(94)90200-3;
 RA O'Reilly M.S., Holmgren L., Shing Y., Chen C., Rosenthal R.A.,
 RA Moses M., Lane W.S., Cao Y., Sage E.H., Folkman J.;
 RT "Angiotatin: a novel angiogenesis inhibitor that mediates the
 RT suppression of metastases by a Lewis lung carcinoma.";
 RL Cell 79:315-328(1994).
 RN [20]
 RP CHARACTERIZATION OF ANGIOTATIN.
 RX MEDLINE=97238710; PubMed=9102221;
 RA Sim B.K., O'Reilly M.S., Liang H., Fortier A.H., He W., Madsen J.W.,
 RA Lapcevic R., Nacy C.A.;
 RT "A recombinant human angiotatin protein inhibits experimental primary
 RT and metastatic cancer.";
 RL Cancer Res. 57:1329-1334(1997).
 RN [21]
 RP INTERACTION WITH CSPG4, AND DOMAIN.
 RX PubMed=10889192; DOI=10.1074/jbc.M002290200;
 RA Goratzki L., Lombardo C.R., Stallcup W.B.;
 RT "Binding of the NC2 proteoglycan to kringle domains modulates the
 RT functional properties of angiotatin and plasmin(ogen).";
 RL J. Biol. Chem. 275:28625-28633(2000).
 RN [22]
 RP INTERACTION WITH AMOT.
 RX PubMed=16043488; DOI=10.1074/jbc.M503915200;
 RA Bratt A., Birot O., Sinha I., Veitonmaeki N., Aase K., Ernkviist M.,
 RA Holmgren L.;
 RT "Angiomotin regulates endothelial cell-cell junctions and cell
 RT motility.";
 RL J. Biol. Chem. 280:34859-34869(2005).
 RN [23]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 374-461.
 RX MEDLINE=92031502; PubMed=1657148;
 RA Mulichak A.M., Tulinsky A., Ravichandran K.G.;
 RT "Crystal and molecular structure of human plasminogen kringle 4
 RT refined at 1.9-A resolution.";

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RL Biochemistry 30:10576-10588 (1991).
RL [24]
Query Match 99.7%; Score 1535; DB 1; Length 810;
Best Local Similarity 99.6%; Pred. No. 4.9e-109;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 VYLSECKTGNGKNGYRGTSKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN 60
DB 98 VYLSECKTGNGKNGYRGTSKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN 157
QY 61 DQGPWCYTTDEPKRYDYCDILLECEBECMHCSENGYDGIKSKTMSGLECOAQDSQSPHAH 120
DB 158 DQGPWCYTTDEPKRYDYCDILLECEBECMHCSENGYDGIKSKTMSGLECOAQDSQSPHAH 217
QY 121 GYIPSPFPNNLKNKNCYCRNPDRELRCWELCDIPRCTTTPPSSGPTYQCLK 180
DB 218 GYIPSPFPNNLKNKNCYCRNPDRELRCWELCDIPRCTTTPPSSGPTYQCLK 277
QY 181 GTGENYRGNAVTVSGHTCOHWSAQTPTHTERTPENFPCKNLDENYCRNPDGKRAPWCHT 240
DB 278 GTGENYRGNAVTVSGHTCOHWSAQTPTHTERTPENFPCKNLDENYCRNPDGKRAPWCHT 337
QY 241 TNSQVRWEYCKIPSCDSSPV 260
DB 338 TNSQVRWEYCKIPSCDSSPV 357
RESULT 2
Q5TEH4 HUMAN PRELIMINARY; PRT; 810 AA.
AC Q5TEH4;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 8.
DE Plasminogen.
GN Name-PLG; ORFNames-RP1-81D.1-001;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Tracey A.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
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CC -----
DR EMBL; AL109933; CAI22908.1; -; Genomic DNA.
DR SMR; Q5TEH4; 562-810.
DR Ensembl; ENSG00000122194; Homo sapiens.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004283; F:plasmin activity; IEA.
DR GO; GO:0007596; P:blood coagulation; IEA.
DR GO; GO:0050874; P:organismal physiological process; IEA.
DR GO; GO:0006508; P:proteolysis; IEA.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR003014; PAN.
DR InterPro; IPR003609; Pan app.
DR InterPro; IPR011358; Peptidase S1.
DR InterPro; IPR001254; Peptidase S1A.
DR InterPro; IPR001314; Peptidase S1A.
DR InterPro; IPR003966; Peptidase_S1A_pp.
DR Pfam; PF00051; Kringle; 5.
DR Pfam; PF00024; PAN 1; 1.
DR Pfam; PF00089; Trypsin; 1.
DR PIRSF; PIRSF001150; plasmin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR01505; PROTHROMBIN.

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DR SMART; SM00130; KR; 5.
DR SMART; SM00473; PAN_AP; 1.
DR SMART; SM00020; TRY_SPC; 1.
DR PROSITE; PS00021; KRINGLE 1; UNKNOWN_5.
DR PROSITE; PS00070; KRINGLE 2; 5.
DR PROSITE; PS00948; PAN; 1.
DR PROSITE; PS02040; TRYPsin DOM; 1.
DR PROSITE; PS00134; TRYPsin HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPsin_SER; 1.
KW Hydrolyase; Kringle; Protease; Serine protease.
SQ SEQUENCE 810 AA; 90569 MW; 8B31CB877CCB3AB6 CRC64;
Query Match 99.7%; Score 1535; DB 2; Length 810;
Best Local Similarity 99.6%; Pred. No. 4.9e-109;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 VYLSECKTGNGKNGYRGTSKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN 60
DB 98 VYLSECKTGNGKNGYRGTSKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN 157
QY 61 DQGPWCYTTDEPKRYDYCDILLECEBECMHCSENGYDGIKSKTMSGLECOAQDSQSPHAH 120
DB 158 DQGPWCYTTDEPKRYDYCDILLECEBECMHCSENGYDGIKSKTMSGLECOAQDSQSPHAH 217
QY 121 GYIPSPFPNNLKNKNCYCRNPDRELRCWELCDIPRCTTTPPSSGPTYQCLK 180
DB 218 GYIPSPFPNNLKNKNCYCRNPDRELRCWELCDIPRCTTTPPSSGPTYQCLK 277
QY 181 GTGENYRGNAVTVSGHTCOHWSAQTPTHTERTPENFPCKNLDENYCRNPDGKRAPWCHT 240
DB 278 GTGENYRGNAVTVSGHTCOHWSAQTPTHTERTPENFPCKNLDENYCRNPDGKRAPWCHT 337
QY 241 TNSQVRWEYCKIPSCDSSPV 260
DB 338 TNSQVRWEYCKIPSCDSSPV 357
RESULT 3
Q5R8X6 PONPY PRELIMINARY; PRT; 810 AA.
AC Q5R8X6;
DT 21-DEC-2004, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 12.
DE Hypothetical protein DKFZp470G2422.
GN Name-DKFZp470G2422;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RG The German cDNA Consortium;
RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RA Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
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CC -----
DR EMBL; CR859622; CAH91784.1; -; mRNA.
DR SMR; Q5R8X6; 185-352, 564-810.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004283; F:plasmin activity; IEA.
DR GO; GO:0007596; P:blood coagulation; IEA.
DR GO; GO:0050874; P:organismal physiological process; IEA.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR003014; PAN.
DR InterPro; IPR003609; Pan_app.

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DR InterPro; IPR011358; Pept S1A Plasmin.
 DR InterPro; IPR001254; Peptidase S1 S6.
 DR InterPro; IPR001314; Peptidase S1A.
 DR InterPro; IPR003966; Peptidase S1A_pp.
 DR Pfam; PF00051; Kringle; 5.
 DR Pfam; PF00024; PAN 1; 1.
 DR Pfam; PF00089; Trypsin; 1.
 DR PIRSF; PIRSF001150; Plasmin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE.
 DR PRINTS; PR01505; PROTHROMBIN.
 DR ProDom; PD000395; Kringle; 5.
 DR SMART; SM00130; KR; 5.
 DR SMART; SM00473; PAN AP; 1.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS00021; KRINGLE_1; UNKNOWN_5.
 DR PROSITE; PS00070; KRINGLE_2; 5.
 DR PROSITE; PS00948; PAN; 1.
 DR PROSITE; PS02040; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR HYDROLASE; Hypothetical protein; Kringle; Protease; Serine protease.
 KW SEQUENCE 810 AA; 90360 MW; 126D530C9942ADD4 CRC64;
 SQ

Query Match 94.7%; Score 1458; DB 2; Length 810;
 Best Local Similarity 95.0%; Pred. No. 3.8e-103;
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 QY 1 VYLSECKTGNGNYRGTWSTKXNGITCQKWSSTSPHRPFSPTATPSEGLEENYCRNPDN 60
 DB 98 VYLSECKTGNGNYRGTWSTKXNGITCQKWSSTSPHRPFSPTATPSEGLEENYCRNPDN 157
 QY 61 DQGPWCYTTDPEKDYDCIILECEBCHMGSGENYDGHKISKTMSGLECQAWDSQSPH 120
 DB 158 DAQGPWCYTTDPEHYDYDCIPECEACMHCSENGYDGHKISKTMSGLECQAWDSQSPH 217
 QY 121 GYIPSKFNKLNKYNCRNPDELPRWCFTDPNKRWELCDIPRCTTPPSSGPTVQCLK 180
 DB 218 GYIPSKFNKLNKYNCRNPDEGPRWCFTDPNKRWELCDIPRCTTPPSSGPTVQCLK 277
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 DB 278 GTGENYRGNVAVTSGHTCQHSQAQTPHTERTPENFPCKNLDENYCRNPDGKAPWCYT 337
 QY 241 TNSQVRWEYCKIPSCDSSPV 260
 DB 338 TNSQVRWEYCKIPSCGSPV 357

RESULT 4

ID PLMN MACMU STANDARD; PRT; 810 AA.
 AC P12545;
 DT 01-OCT-1989, integrated into UniProtKB/Swiss-Prot.
 DT 01-OCT-1989, sequence version 1.
 DT 07-MAR-2006, entry version 65.
 DE Plasminogen precursor (EC 3.4.21.7) [Contains: Plasmin heavy chain A;
 DE Activation peptide; Plasmin heavy chain A, short form; Plasmin light
 DE chain B].
 OS Name=PLG;
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 OC Cercopithecoidea; Cercopithecinae; Macaca.
 OX NCBI_TaxID=9544;
 RN NUCLEOTIDE SEQUENCE [MRNA].
 RP MEDLINE=89174660; PubMed=2925643;
 RX Tomlinson J.E., McLean J.W., Lawn R.M.;
 RA "Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of
 RT synthesis.";
 RL J. Biol. Chem. 264:5957-5965(1989).
 CC -!- FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as

a proteolytic factor in a variety of other processes including embryonic development, tissue remodeling, tumor invasion, and inflammation; in ovulation it weakens the walls of the Graafian follicle. It activates the urokinase-type plasminogen activator, collagenases and several complement zymogens, such as C1 and C5. It cleaves fibrin, fibronectin, thrombospondin, laminin and von Willebrand factor. Its role in tissue remodeling and tumor invasion may be modulated by CSPG4.
 CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;
 CC higher selectivity than trypsin. Converts fibrin into soluble products.
 CC -!- ENZYME REGULATION: Converted into plasmin by plasminogen activators, both plasminogen and its activator being bound to fibrin. Activated with catalytic amounts of streptokinase.
 CC -!- SUBUNIT: Interacts with CSPG4 (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted protein.
 CC -!- DOMAIN: Kringle domains mediate interaction with CSPG4 (By similarity).
 CC -!- PTM: In the presence of the inhibitor, the activation involves only cleavage after Arg-580, yielding two chains held together by two disulfide bonds. In the absence of the inhibitor, the activation involves additionally the removal of the activation peptide (By similarity).
 CC -!- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin immediately after dissociation from the clot.
 CC -!- MISCELLANEOUS: In the presence of the inhibitor, the activation involves only cleavage after Arg-580, resulting in 2 chains held together by 2 disulfide bonds. Without the inhibitor, the activation involves also removal of the activation peptide.
 CC -!- SIMILARITY: Belongs to the peptidase S1 family. Plasminogen subfamily.
 CC -!- SIMILARITY: Contains 5 kringle domains.
 CC -!- SIMILARITY: Contains 1 PAN domain.
 CC -!- SIMILARITY: Contains 1 peptidase S1 domain.
 CC
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 CC
 CC EMBL; J04697; AAA36901.1; -; mRNA.
 DR PIR; B32869; B30848.
 DR HSSP; P00747; 1BUI.
 DR SMR; P12545; 184-352, 564-810.
 DR MEROPS; S01.233; -.
 DR LinkHub; P12545; -.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR003014; PAN.
 DR InterPro; IPR003609; Pan app.
 DR InterPro; IPR011358; Pept S1A Plasmin.
 DR InterPro; IPR001254; Peptidase S1 S6.
 DR InterPro; IPR001314; Peptidase S1A.
 DR InterPro; IPR003966; Peptidase S1A_pp.
 DR Pfam; PF00051; Kringle; 5.
 DR Pfam; PF00024; PAN 1; 1.
 DR Pfam; PF00089; Trypsin; 1.
 DR PIRSF; PIRSF001150; Plasmin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE.
 DR PRINTS; PR01505; PROTHROMBIN.
 DR ProDom; PD000395; Kringle; 5.
 DR SMART; SM00130; KR; 5.
 DR SMART; SM00473; PAN AP; 1.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS00021; KRINGLE_1; 5.
 DR PROSITE; PS00070; KRINGLE_2; 5.
 DR PROSITE; PS00948; PAN; 1.
 DR PROSITE; PS02040; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Blood coagulation; Fibrinolysis; Glycoprotein; Hydrolase; Kringle;
 RT Signalase; Repeat; Serine protease; Signal; tissue remodeling; Zymogen.
 FT SIGNAL 1 19
 FT CHAIN 20 810 Plasminogen.
 FT /FTID=PRO_0000028059.

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FT CHAIN 20 580 Plasmin heavy chain A.
FT PEPTIDE 20 96 /FTid=PRO_0000028060.
FT 96 Activation peptide.
FT CHAIN 97 580 /FTid=PRO_0000028061.
FT 580 Plasmin heavy chain A, short form.
FT CHAIN 581 810 /FTid=PRO_0000028062.
FT 810 Plasmin light chain B.
FT 810 /FTid=PRO_0000028063.
FT DOMAIN 20 98 PAN.
FT DOMAIN 103 181 Kringle 1.
FT DOMAIN 184 262 Kringle 2.
FT DOMAIN 275 352 Kringle 3.
FT DOMAIN 377 454 Kringle 4.
FT DOMAIN 481 560 Kringle 5.
FT DOMAIN 581 808 Peptidase S1.
FT ACT_SITE 622 622 Charge relay system.
FT ACT_SITE 665 665 Charge relay system.
FT ACT_SITE 760 760 Charge relay system.
FT BINDING 134 134 Fibrin.
FT BINDING 136 136 Fibrin.
FT BINDING 136 136 Omega-aminocarboxylic acids.
FT BINDING 136 136 Omega-aminocarboxylic acids.
FT BINDING 158 158 Omega-aminocarboxylic acids.
FT BINDING 172 172 Omega-aminocarboxylic acids.
FT BINDING 432 432 Omega-aminocarboxylic acids.
FT BINDING 445 445 Omega-aminocarboxylic acids.
FT CARBOHYD 365 365 O-linked (GalNAc...) (By similarity).
FT DISULFID 49 73 By similarity.
FT DISULFID 53 61 By similarity.
FT DISULFID 103 181 By similarity.
FT DISULFID 124 164 By similarity.
FT DISULFID 152 176 By similarity.
FT DISULFID 185 262 By similarity.
FT DISULFID 188 316 By similarity.
FT DISULFID 206 245 By similarity.
FT DISULFID 234 257 By similarity.
FT DISULFID 275 352 By similarity.
FT DISULFID 296 335 By similarity.
FT DISULFID 324 347 By similarity.
FT DISULFID 377 454 By similarity.
FT DISULFID 398 437 By similarity.
FT DISULFID 426 449 By similarity.
FT DISULFID 481 560 By similarity.
FT DISULFID 502 543 By similarity.
FT DISULFID 531 555 By similarity.
FT DISULFID 567 685 Interchain (between A and B chains) (By similarity).
FT 577 585 Interchain (between A and B chains) (By similarity).
FT 607 623 By similarity.
FT DISULFID 699 766 By similarity.
FT DISULFID 729 745 By similarity.
FT DISULFID 756 784 By similarity.
SQ SEQUENCE 810 AA; 90255 MW; A75E1C51A1A0F24A CRC64;

Query Match 93.6%; Score 1442; DB 1; Length 810;
Best Local Similarity 93.1%; Pred. No. 6.4e-102;
Matches 242; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGNYRTGKTKNGITCQKWSSTSPHRPFSPTHSEGLEENYCRNPDN 60
DB 98 VYLSECKTGNGNYRTGKTKNGITCQKWSSTSPHRPFSPTHSEGLEENYCRNPDN 157
QY 61 DPQGPWCYTTDPKRYDYCDILECEECMHCSENGYDGKISKTMGLECQAWDSQSPH 120
DB 158 DGQGPWCYTTDPKRYDYCDILECEECMHCSENGYDGKISKTMGLECQAWDSQSPH 217
QY 121 GYIPSKFPNNLKNKYCRNPDRELRCWCTTDPNKRWELCDIPRCTTTPPPSGTTC 180
DB 218 GYIPSKFPNNLKNKYCRNPDGEPRPWCFTTDPNKRWELCDIPRCTTTPPPSGTTC 277
QY 181 GTGNYRGNAVTVSGHTCOHWSAQTPHTHTPENFPCKNLNDENYCRNPDGKRA 240
DB 278 GTGNYRGNAVTVSGHTCHGWSAQTPHTHTPENFPCKNLNDENYCRNPDGKRA 337
```

```
QY 241 TNSQVRWEYCKIPSCDSSPV 260
DB 338 TNSQVRWEYCKIPSCDSSPV 357

RESULT 5
Q8WRI1 CANFA PRELIMINARY; PRT; 359 AA.
AC Q8WRI1;
DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2002, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE Plasminogen (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]_TaxID=9615;
RP NUCLEOTIDE SEQUENCE.
RA Pirie-Shepherd S.R., Coffman K.T., Resnick D., Chan R., Kisker O.,
RA Folkman J., Waters D.J.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; AY069985; AAL58519.1; -; mRNA.
DR HSSP; P00747; 1PMK.
DR SMR; Q8WRI1; 87-255.
DR Ensembl; ENSCARG0000000759; Canis familiaris.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004252; F:serine-type endopeptidase activity; IEA.
DR GO; GO:0007596; P:blood coagulation; IEA.
DR GO; GO:006508; P:proteolysis; IEA.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR003966; Peptidase_S1A_pp.
DR Pfam; PF00551; Kringle; 4.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR01505; PROTHROMBIN.
DR ProDom; PD000395; Kringle; 4.
DR SMART; SM00130; KB; 4.
DR PROSITE; PS00021; KRINGLE_1; 4.
DR PROSITE; PSS0070; KRINGLE_2; 4.
KW Kringle.
FT NON_TER 1 1
FT NON_TER 359 359
SQ SEQUENCE 359 AA; 41173 MW; 776D35F4AB0BDD9E CRC64;

Query Match 84.8%; Score 1306; DB 2; Length 359;
Best Local Similarity 81.2%; Pred. No. 6.9e-92;
Matches 211; Conservative 23; Mismatches 26; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGNYRTGKTKNGITCQKWSSTSPHRPFSPTHSEGLEENYCRNPDN 60
DB 1 IYLSECKTGNGTYRTGTMKTNDVACQKWSNPHKPNYTPKHPLGLEENYCRNPDN 60
QY 61 DPQGPWCYTTDPKRYDYCDILECEECMHCSENGYDGKISKTMGLECQAWDSQSPH 120
DB 61 DENGWPCTTNDVDFDYNIPCECEECMHCSENGYEGKISKTMGLECQAWNSQTPH 120
QY 121 GYIPSKFPNNLKNKYCRNPDRELRCWCTTDPNKRWELCDIPRCTTTPPPSGTTC 180
DB 121 GYIPSKFPNNLKNKYCRNPDGEPRPWCFTTDPNKRWELCDIPRCTTTPPPSGTTC 180
QY 181 GTGNYRGNAVTVSGHTCOHWSAQTPHTHTPENFPCKNLNDENYCRNPDGKRA 240
DB 181 GRGESYRGKSVTVSGHTCOHWSAQTPHTHTPENFPCKNLNDENYCRNPDGKRA 240
QY 241 TNSQVRWEYCKIPSCDSSPV 260
DB 241 TNSQVRWEYCKIPSCDSSPV 357
```

RESULT 6		Distributed under the Creative Commons Attribution-NoDerivs License	
PLMN_RAT	PLMN_RAT	STANDARD;	PRT; 812 AA.
ID	Q01177; Q9ROW3;		
DT	01-APR-1993, integrated into UniProtKB/Swiss-Prot.		
DT	31-AUG-2004, sequence version 2.		
DT	07-WAR-2006, entry version 50.		
DE	Plasminogen precursor (EC 3.4.21.7) [Contains: Plasmin heavy chain A;		
DE	Activation peptide; Angiostatin; Plasmin heavy chain A, short form;		
DE	Plasmin light chain B].		
GN	Name=Plg;		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;		
OC	Muroidea; Muridae; Murinae; Rattus.		
OX	NCBI_TaxID=10116;		
RN	[1] _TaxID=10116;		
RP	NUCLEOTIDE SEQUENCE [MRNA].		
RC	TISSUE=Liver;		
RA	Bangert K., Johnsen A.H., Thorsen S.;		
RT	"Rat plasminogen: cDNA and gene structure.";		
RL	Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.		
RP	NUCLEOTIDE SEQUENCE [MRNA] OF 343-511.		
RC	TISSUE=Liver;		
RX	MEDLINE=91250378; PubMed=1645711;		
RA	Kanalas J.J., Makker S.P.;		
RT	"Identification of the rat Heymann nephritis autoantigen (GP330) as a		
RT	receptor site for plasminogen.";		
RL	J. Biol. Chem. 266:10825-10829(1991).		
CC	-!- FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as		
CC	a proteolytic factor in a variety of other processes including		
CC	embryonic development, tissue remodeling, tumor invasion, and		
CC	inflammation; in ovulation it weakens the walls of the Graafian		
CC	follicle. It activates the urokinase-type plasminogen activator,		
CC	collagenases and several complement zymogens, such as C1 and C5.		
CC	It cleaves fibrin, fibronectin, thrombospondin, laminin and von		
CC	Willebrand factor. Its role in tissue remodeling and tumor		
CC	invasion may be modulated by CSPG4.		
CC	-!- FUNCTION: Angiostatin is an angiogenesis inhibitor that blocks		
CC	neovascularization and growth of experimental primary and		
CC	metastatic tumors in vivo (By similarity).		
CC	-!- CATALYTIC ACTIVITY: Preferential cleavage: Lys- -Xaa > Arg- -Xaa;		
CC	higher selectivity than trypsin. Converts fibrin into soluble		
CC	products.		
CC	-!- ENZYME REGULATION: Converted into plasmin by plasminogen		
CC	activators, both plasminogen and its activator being bound to		
CC	fibrin. Cannot be activated with streptokinase.		
CC	-!- SUBUNIT: Interacts with CSPG4 and AMO1 (By similarity).		
CC	-!- SUBCELLULAR LOCATION: Secreted protein.		
CC	-!- DOMAIN: Kringle domains mediate interaction with CSPG4 (By		
CC	similarity).		
CC	-!- PTM: In the presence of the inhibitor, the activation involves		
CC	only cleavage after Arg-581, yielding two chains held together by		
CC	two disulfide bonds. In the absence of the inhibitor, the		
CC	activation involves additionally the removal of the activation		
CC	peptide (By similarity).		
CC	-!- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin		
CC	immediately after dissociation from the clot.		
CC	-!- MISCELLANEOUS: In the presence of the inhibitor, the activation		
CC	involves only cleavage after Arg-581, resulting in 2 chains held		
CC	together by 2 disulfide bonds. Without the inhibitor, the		
CC	activation involves also removal of the activation peptide (By		
CC	similarity).		
CC	-!- SIMILARITY: Belongs to the peptidase S1 family. Plasminogen		
CC	subfamily.		
CC	-!- SIMILARITY: Contains 5 kringle domains.		
CC	-!- SIMILARITY: Contains 1 PAN domain.		
CC	-!- SIMILARITY: Contains 1 peptidase S1 domain.		
CC	-----		
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms		

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CC	EMBL; AJ242649; CAB46014.1; -; mRNA.
CC	EMBL; M62832; AAA41884.1; -; mRNA.
DR	PIR; A40522; A40522.
DR	HSSP; P00747; LPMK.
DR	SMR; Q01177; 565-812.
DR	MEROPS; S01.233; -.
DR	Ensembl; ENSRNOG0000017223; Rattus norvegicus.
DR	RGD; 619893; Plg.
DR	InterPro; IPR000001; Kringle.
DR	InterPro; IPR003014; PAN.
DR	InterPro; IPR003609; Pan_app.
DR	InterPro; IPR011358; Pept_S1A_Plasmin.
DR	InterPro; IPR001254; Peptidase_S1_S6.
DR	InterPro; IPR001314; Peptidase_S1A.
DR	InterPro; IPR003966; Peptidase_S1A_pp.
DR	Pfam; PF00051; Kringle; 5.
DR	Pfam; PF00024; PAN_1; 1.
DR	Pfam; PF00089; TRYPSIN; 1.
DR	PIRSF; PIRSF001150; Plasmin; 1.
DR	PRINTS; PR00722; CHYMOTRYPSIN.
DR	PRINTS; PR00018; KRINGLE.
DR	PRINTS; PR01505; PROTHROMBIN.
DR	ProDom; PD000395; Kringle; 1.
DR	SMART; SM00130; KR; 5.
DR	SMART; SM00473; PAN_AP; 1.
DR	SMART; SM00020; Tryp_SPC; 1.
DR	PROSITE; PS00021; KRINGLE_1; 5.
DR	PROSITE; PS00070; KRINGLE_2; 5.
DR	PROSITE; PS00948; PAN; 1.
DR	PROSITE; PS0240; TRYPSIN_DOM; 1.
DR	PROSITE; PS00134; TRYPSIN_HIS; 1.
DR	PROSITE; PS00135; TRYPSIN_SER; 1.
KW	Blood coagulation; Fibrinolysis; Hydrolase; Kringle; Protease; Repeat;
KW	Serine protease; Signal; Tissue remodeling; Zymogen.
FT	SIGNAL 1 19 By similarity.
FT	CHAIN 20 812 Plasminogen.
FT	FTID=PRO_0000028079.
FT	Plasmin heavy chain A.
FT	/FTID=PRO_0000028080.
FT	Activation peptide (By similarity).
FT	/FTID=PRO_0000028081.
FT	Plasmin heavy chain A, short form.
FT	/FTID=PRO_0000028082.
FT	Angiostatin.
FT	/FTID=PRO_0000028083.
FT	Plasmin light chain B.
FT	/FTID=PRO_0000028084.
FT	PAN.
FT	DOMAIN 20 98 Kringle 1.
FT	DOMAIN 102 181 Kringle 2.
FT	DOMAIN 184 262 Kringle 3.
FT	DOMAIN 274 352 Kringle 4.
FT	DOMAIN 375 454 Kringle 5.
FT	DOMAIN 480 560 Kringle 5.
FT	DOMAIN 582 810 Peptidase S1.
FT	ACT_SITE 624 824 Charge relay system (By similarity).
FT	ACT_SITE 667 762 Charge relay system (By similarity).
FT	DISULFID 49 73 By similarity.
FT	DISULFID 53 61 By similarity.
FT	DISULFID 103 181 By similarity.
FT	DISULFID 124 164 By similarity.
FT	DISULFID 152 176 By similarity.
FT	DISULFID 185 262 By similarity.
FT	DISULFID 188 316 By similarity.
FT	DISULFID 206 245 By similarity.
FT	DISULFID 234 257 By similarity.
FT	DISULFID 275 352 By similarity.
FT	DISULFID 296 335 By similarity.
FT	DISULFID 324 347 By similarity.
FT	DISULFID 376 454 By similarity.
FT	DISULFID 397 437 By similarity.

FT DISULFID 425 449 By similarity.
 FT DISULFID 481 560 By similarity.
 FT DISULFID 502 543 By similarity.
 FT DISULFID 531 555 By similarity.
 FT DISULFID 568 687 Interchain (between A and B chains) (By similarity)
 FT DISULFID 578 586 Interchain (between A and B chains) (By similarity)
 FT DISULFID 609 625 By similarity.
 FT DISULFID 701 768 By similarity.
 FT DISULFID 731 747 By similarity.
 FT DISULFID 758 786 By similarity.
 FT CONFLICT 418 418 A -> S (in Ref. 2).
 SQ SEQUENCE 812 AA; 90536 MW; 8C703C51410EBC9E CRC64;

Query Match 84.4%; Score 1299; DB 1; Length 812;
 Best Local Similarity 82.6%; Pred. No. 5.8e-91;
 Matches 213; Conservative 21; Mismatches 24; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGNYRGTMSTKNGITCQKWSSTSPHPRFSPATHPSEGLEENYCRNPDN 60
 DB 98 VYLSECKTGIGKGYRGTMSTKNGITCQKWSSTSPHPRFSPATHPSEGLEENYCRNPDN 157

QY 61 DPQGPWCYTTDPKRYDYCDILECEBECMHCSENGYDGIKISKTMSGLCQAWDSQSPHAF 120
 DB 158 DQGPWCYTTDPQRYEYCNIPCEBECMHCSENGYDGIKISKTMSGLCQAWDSQSPHAF 217

QY 121 GYIPSKFPNKLKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTTPPSSGPTYQCLK 180
 DB 218 GYIPAKFPNKLKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTTPPSSGPTYQCLK 277

QY 181 GTGNYRGNAVTVSGHTCQHSQAOTPHRTPTNPFCNLDENYCRNPDGKRAPWCHT 240
 DB 278 GRGNYRGTVSVTASGKTQCRWSEQTTPHRTPTNPFCNLDENYCRNPDGKRAPWCHT 337

QY 241 TNSQVRWEYCKIPSCDSS 258
 DB 338 TDSQLRWEYCEIPSCSS 355

RESULT 7
 Q5BK6 RAT PRELIMINARY; PRT; 812 AA.
 AC Q5BK6;
 DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
 DT 10-MAY-2005, sequence version 1.
 DT 07-FEB-2006, entry version 10.
 DE Plasminogen.
 GN Name:Plg;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Rattus.
 OX NCBI_TaxId=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toehiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fackey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakešley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J.J., Schmutz J., Myers R.M.,

RESULT 8

RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,
 RA Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Liver;
 RG NIH MGC Project;
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
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 CC -----
 CC EMBL; BC091135; AA91135.1; -; mRNA.
 DR SMR; Q5BK6; 565-812.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0004283; F:plasmin activity; IEA.
 DR GO; GO:0007596; P:blood coagulation; IEA.
 DR GO; GO:0050874; P:organismal physiological process; IEA.
 DR GO; GO:0008508; P:proteolysis; IEA.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR003014; PAN.
 DR InterPro; IPR003609; Pan app.
 DR InterPro; IPR011358; Pept_SIA_Plasmin.
 DR InterPro; IPR001254; Peptidase_S1_S6.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR InterPro; IPR003966; Peptidase_S1A_pp.
 DR Pfam; PF00051; Kringle; 5.
 DR Pfam; PF00024; PAN 1; 1.
 DR Pfam; PF00089; Trypsin; 1.
 DR PIRSF; PIRSF001150; Plasmin; 1.
 DR PRINTS; PRO00722; CHYMOTRYPSIN.
 DR PRINTS; PRO0018; KRINGLE.
 DR PRINTS; PRO1505; PROTHROMBIN.
 DR SMART; SM00130; KR; 5.
 DR SMART; SM00473; PAN_AP; 1.
 DR SMART; SM00020; TRY_SPC; 1.
 DR PROSITE; PS00021; KRINGLE_1; UNKNOWN_5.
 DR PROSITE; PS00070; KRINGLE_2; 5.
 DR PROSITE; PS00948; PAN; 1.
 DR PROSITE; PS0240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Hydrolase; Kringle; Protease; Serine protease.
 SQ SEQUENCE 812 AA; 90536 MW; 8C703C51410EBC9E CRC64;

Query Match 84.4%; Score 1299; DB 2; Length 812;
 Best Local Similarity 82.6%; Pred. No. 5.8e-91;
 Matches 213; Conservative 21; Mismatches 24; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGNYRGTMSTKNGITCQKWSSTSPHPRFSPATHPSEGLEENYCRNPDN 60
 DB 98 VYLSECKTGIGKGYRGTMSTKNGITCQKWSSTSPHPRFSPATHPSEGLEENYCRNPDN 157

QY 61 DPQGPWCYTTDPKRYDYCDILECEBECMHCSENGYDGIKISKTMSGLCQAWDSQSPHAF 120
 DB 158 DQGPWCYTTDPQRYEYCNIPCEBECMHCSENGYDGIKISKTMSGLCQAWDSQSPHAF 217

QY 121 GYIPSKFPNKLKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTTPPSSGPTYQCLK 180
 DB 218 GYIPAKFPNKLKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTTPPSSGPTYQCLK 277

QY 181 GTGNYRGNAVTVSGHTCQHSQAOTPHRTPTNPFCNLDENYCRNPDGKRAPWCHT 240
 DB 278 GRGNYRGTVSVTASGKTQCRWSEQTTPHRTPTNPFCNLDENYCRNPDGKRAPWCHT 337

QY 241 TNSQVRWEYCKIPSCDSS 258
 DB 338 TDSQLRWEYCEIPSCSS 355

PLMN_PIG
 ID PLMN_PIG STANDARD; PRT; 790 AA.
 AC P06867;
 DT 01-JAN-1988, integrated into UniProtKB/Swiss-Prot.
 DT 01-FEB-1991, sequence version 2.
 DT 07-MAR-2006, entry version 66.
 DE Plasmicogen precursor (EC 3.4.21.7) [Contains: Plasmicogen heavy chain A;
 DE Activation peptide; Plasmicogen heavy chain A, short form; Plasmicogen light
 DE chain B].
 GN Name=PLG;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
 OC Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP PROTEIN SEQUENCE OF 1-560.
 RA Schaller J., Marti T., Roessel S.J., Kaempfer U., Rickli E.E.;
 RT "Amino acid sequence of the heavy chain of porcine plasmin. Comparison
 RT of the carbohydrate attachment sites with the human and bovine
 RT species.";
 RL Fibrinolysis 1:91-102(1987).
 RN [2]
 RP PROTEIN SEQUENCE OF 450-790.
 RX MEDLINE=85203907; PubMed=3846533;
 RA Marti T., Schaller J., Rickli E.E.;
 RT "Determination of the complete amino-acid sequence of porcine
 RT miniplasminogen.";
 RL Eur. J. Biochem. 149:279-285(1985).
 RN [3]
 RP CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=88185329; PubMed=3356193;
 RA Marti T., Schaller J., Rickli E.E., Schmid K., Kamerling J.P.,
 RA Gerwig G.J., van Halbeek H., Vliegthart J.F.;
 RT "The N- and O-linked carbohydrate chains of human, bovine and porcine
 RT plasminogen. Species specificity in relation to sialylation and
 RT fucosylation patterns.";
 RL Eur. J. Biochem. 173:57-63(1988).
 CC -!- FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as
 CC a proteolytic factor in a variety of other processes including
 CC embryonic development, tissue remodeling, tumor invasion, and
 CC inflammation; in ovulation it weakens the walls of the Graafian
 CC follicle. It activates the urokinase-type plasminogen activator,
 CC collagenases and several complement zymogens, such as C1 and C5.
 CC It cleaves fibrin, fibronectin, thrombospondin, laminin and von
 CC Willebrand factor. Its role in tissue remodeling and tumor
 CC invasion may be modulated by CSPG4.
 CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Lys-[Xaa > Arg]-[Xaa;
 CC higher selectivity than trypsin. Converts fibrin into soluble
 CC products.
 CC -!- ENZYME REGULATION: Converted into plasmin by plasminogen
 CC activators, both plasminogen and its activator being bound to
 CC fibrin. Cannot be activated with streptokinase.
 CC -!- SUBUNIT: Interacts with CSPG4 (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted protein.
 CC -!- DOMAIN: Kringle domains mediate interaction with CSPG4 (By
 CC similarity).
 CC -!- PTM: N-linked glycan contains N-acetylglucosamine, sialic acid and
 CC is core fucosylated. O-linked glycans consist of Gal-GalNAc
 CC disaccharide which is modified with up to 2 sialic acid residues
 CC (microheterogeneity).
 CC -!- PTM: In the presence of the inhibitor, the activation involves
 CC only cleavage after Arg-560, yielding two chains held together by
 CC two disulfide bonds. In the absence of the inhibitor, the
 CC activation involves additionally the removal of the activation
 CC peptide (By similarity).
 CC -!- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin
 CC immediately after dissociation from the clot.
 CC -!- SIMILARITY: Belongs to the peptidase S1 family. Plasminogen
 CC subfamily.
 CC -!- SIMILARITY: Contains 5 kringle domains.
 CC -!- SIMILARITY: Contains 1 PAN domain.
 CC -!- SIMILARITY: Contains 1 peptidase S1 domain.

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 CC -----
 CC PIR; S03733; PLPG.
 CC HSSP; P06867; 1BUI.
 CC SMR; P06867; 544-790.
 CC MEROPS; S01.233; -.
 CC GlycoSuiteDB; P06867; -.
 CC InterPro; IPR000001; Kringle.
 CC InterPro; IPR003014; PAN.
 CC InterPro; IPR003609; Pan app.
 CC InterPro; IPR011358; Pept_S1A_Plasmin.
 CC InterPro; IPR001354; Peptidase_S1_S6.
 CC InterPro; IPR001314; Peptidase_S1A.
 CC InterPro; IPR003966; Peptidase_S1A_pp.
 CC Pfam; PF00051; Kringle; 5.
 CC Pfam; PF00024; PAN_1; 1.
 CC PIRSF; PIRSF001150; Plasmin; 1.
 CC PRINTS; PRO0722; CHYMOTRYPSIN.
 CC PRINTS; PRO0018; KRINGLE.
 CC PRINTS; PRO1505; PROTHROMBIN.
 CC ProDom; PD000395; Kringle; 5.
 CC SMART; SM00130; KR; 5.
 CC SMART; SM00473; PAN_AP; 1.
 CC SMART; SM00020; Tryp_Spc; 1.
 CC PROSITE; PS00021; KRINGLE_1; 5.
 CC PROSITE; PS00070; KRINGLE_2; 5.
 CC PROSITE; PS00948; PAN; 1.
 CC PROSITE; PS0240; TRYPSIN_DOM; 1.
 CC PROSITE; PS00134; TRYPSIN_HIS; FALSE_NEG.
 CC PROSITE; PS00135; TRYPSIN_SER; 1.
 CC Blood coagulation; Direct protein sequencing; Fibrinolysis;
 CC Glycoprotein; Hydrolysis; Protease; Repeat; Serine protease;
 CC Tissue remodeling; Zymogen.
 CC CHAIN 1 560 plasmin heavy chain A.
 CC PEPTIDE 1 78 /FTID=PRO_000028075.
 CC CHAIN 79 560 /FTID=PRO_000028076.
 CC CHAIN 561 790 /FTID=PRO_000028077.
 CC DOMAIN 1 79 /FTID=PRO_000028078.
 CC DOMAIN 84 162 Kringle 1.
 CC DOMAIN 166 243 Kringle 2.
 CC DOMAIN 256 333 Kringle 3.
 CC DOMAIN 358 435 Kringle 4.
 CC DOMAIN 461 540 Kringle 5.
 CC DOMAIN 561 788 Peptidase S1.
 CC ACT_SITE 602 602 Charge relay system.
 CC ACT_SITE 645 645 Charge relay system.
 CC ACT_SITE 740 740 Charge relay system.
 CC CARBOHYD 289 289 N-linked (GlcNAc...).
 CC CARBOHYD 340 340 /FTID=CAR_000019.
 CC DISULFID 30 54 O-linked (GalNAc...).
 CC DISULFID 34 42 /FTID=CAR_000020.
 CC DISULFID 84 162 By similarity.
 CC DISULFID 105 145 By similarity.
 CC DISULFID 133 157 By similarity.
 CC DISULFID 166 243 By similarity.
 CC DISULFID 169 297 By similarity.
 CC DISULFID 187 226 By similarity.
 CC DISULFID 215 238 By similarity.
 CC DISULFID 256 333 By similarity.
 CC DISULFID 277 316 By similarity.
 CC DISULFID 305 328 By similarity.
 CC DISULFID 358 435 By similarity.
 CC DISULFID 379 418 By similarity.
 CC DISULFID 407 430 By similarity.

RESULT 11

PLMN	MOUSE	
ID	PLMN	MOUSE STANDARD; PRT; 812 AA.
AC	P20918;	O8CIS2; Q91WJ5;
DT	01-FEB-1991,	integrated into UniProtKB/Swiss-Prot.
DT	30-MAY-2003,	sequence version 2.
DT	07-MAR-2006,	entry version 76.
DE	Plasminogen precursor (EC 3.4.21.7)	[Contains: Plasmin heavy chain A;
DE	Activation peptide; Angiostatatin;	Plasmin heavy chain A, short form;
DE	Plasmin light chain B].	
GN	Name=Plg;	
GN	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata;	Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Euarchontoglires;	Glires; Rodentia; Sciurognathi;
OC	Muridea; Muridae; Murinae; Mus.	
OX	NCBI_TaxID=10090;	
RN	[1]	
RN	NUCLEOTIDE SEQUENCE.	
RX	MEDLINE=91184812; PubMed=2081600;	
RX	Degen S.J., Bell S.M., Schaefer L.A., Elliott R.W.;	
RT	"Characterization of the cDNA coding for mouse plasminogen and	
RT	localization of the gene to mouse chromosome 17.";	
RL	Genomics 8:49-61(1990).	
RN	[2]	
RN	NUCLEOTIDE SEQUENCE.	
RC	STRAIN=129/Sv;	
RA	Brathwaite M., Waeltz P., Qian Y., Dudekula D., Schlessinger D.,	
RA	Nagaraja R.;	
RT	"Genomic sequence analysis in the mouse t-complex region.";	
RT	Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.	
RN	[3]	
RN	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].	
RC	TISSUE=Liver;	
RX	MEDLINE=223388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;	
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,	
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,	
RA	Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,	
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,	
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,	
RA	Scapleton M., Soares M.B., Bonaldo M.P., Casavert T.L., Scheetz T.E.,	
RA	Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,	
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,	
RA	Ragak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,	
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	
RA	Villañon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	
RA	Fahy J., Hulton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,	
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,	

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzyzanski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

[4]

NUCLEOTIDE SEQUENCE OF 1-16.

STRAIN=129/SVJ; TISSUE=Liver;

BMEDLINE=22254843; PubMed=12149246; DOI=10.1074/jbc.M202509200;

Manhach F.G., Gutierrez A., Fowler B.J., Bugge T.H., Degen J.L., Parmer R.J., Miles L.A.;

"Localization of regulatory elements mediating constitutive and cytokine-stimulated plasminogen gene expression.";

J. Biol. Chem. 277:38579-38588 (2002).

[5]

CHARACTERIZATION OF ANGIOSTATIN, AND PARTIAL PROTEIN SEQUENCE.

MEDLINE=95042728; PubMed=7525077; DOI=10.1016/0092-8674(94)90200-3;

O'Reilly M.S., Holmgren L., Shing Y., Chen C., Rosenchal R.A., Moses M., Lane W.S., Cao Y., Sage E.H., Folkman J.;

"Angiostatins: a novel angiogenesis inhibitor that mediates the suppression of metastases by a Lewis lung carcinoma.";

Cell 79:315-328 (1994).

-I- FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as a proteolytic factor in a variety of other processes including embryonic development, tissue remodeling, tumor invasion, and inflammation; in ovulation it weakens the walls of the Graafian follicle. It activates the urokinase-type plasminogen activator, collagenases and several complement zymogens, such as C1 and C5. It cleaves fibrin, fibrinectin, thrombospondin, laminin and von Willebrand factor. Its role in tissue remodeling and tumor invasion may be modulated by CSPG4.

-I- FUNCTION: Angiostatin is an angiogenesis inhibitor that blocks neovascularization and growth of experimental primary and metastatic tumors in vivo.

-I- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa; higher selectivity than trypsin. Converts fibrin into soluble products.

-I- ENZYME REGULATION: Converted into plasmin by plasminogen activators, both plasminogen and its activator being bound to fibrin. Cannot be activated with streptokinase.

-I- SUBUNIT: Interacts with CSPG4 and AMOT (By similarity).

-I- SUBCELLULAR LOCATION: Secreted protein.

-I- DOMAIN: Kringle domains mediate interaction with CSPG4 (By similarity).

-I- PTM: In the presence of the inhibitor, the activation involves only cleavage after Arg-581, yielding two chains held together by two disulfide bonds. In the absence of the inhibitor, the activation involves additionally the removal of the activation peptide (By similarity).

-I- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin immediately after dissociation from the clot.

-I- MISCELLANEOUS: In the presence of the inhibitor, the activation involves only cleavage after Arg-581, resulting in 2 chains held together by 2 disulfide bonds. Without the inhibitor, the activation involves also removal of the activation peptide.

-I- SIMILARITY: Belongs to the peptidase S1 family. Plasminogen subfamily.

-I- SIMILARITY: Contains 5 kringle domains.

-I- SIMILARITY: Contains 1 PAN domain.

-I- SIMILARITY: Contains 1 peptidase S1 domain.

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ENBL; J04766; AAA50168.1; -; mRNA.

DR ENBL; AF481053; AAM22156.1; -; Genomic_DNA.

DR ENBL; BC014773; AAH14773.1; -; mRNA.

DR ENBL; BC057186; AAH57186.1; -; mRNA.

DR ENBL; AY134430; AAN15805.1; -; Genomic_DNA.

DR PIR; A38514; PLMS.

DR HGSP; P00747; 1BU1.

DR PIR; P20918; 566-812.
 DR MEROPS; S01.233; -.
 DR Ensembl; ENSMUSG0000059481; Mus musculus.
 DR MGI; MGI:97620; PIG.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0006915; P:apoptosis; IDA.
 DR GO; GO:0006917; P:induction of apoptosis; IDA.
 DR GO; GO:0046716; P:muscle maintenance; IMP.
 DR GO; GO:0045445; P:myoblast differentiation; IMP.
 DR GO; GO:0016525; P:negative regulation of angiogenesis; TAS.
 DR GO; GO:0042246; P:tissue regeneration; IMP.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR003014; PAN.
 DR InterPro; IPR003609; Pan app.
 DR InterPro; IPR011358; Pept_S1A_plasmin.
 DR InterPro; IPR001254; Peptidase_S1_S6.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR InterPro; IPR003966; Peptidase_S1A_pp.
 DR Pfam; PF00051; Kringle; 5.
 DR Pfam; PF00024; PAN 1; 1.
 DR Pfam; PF00089; Trypsin; 1.
 DR FIRSF; FIRSF001150; Plasmin; 1.
 DR PRINTS; PRO0722; CHYMOTRYPSIN.
 DR PRINTS; PRO0018; KRINGLE.
 DR PRINTS; PRO1505; PROTHROMBIN.
 DR ProDom; PD000395; Kringle; 5.
 DR SMART; SM00130; KR; 5.
 DR SMART; SM00473; PAN_AP; 1.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS00021; KRINGLE 1; 5.
 DR PROSITE; PS00070; KRINGLE_2; 5.
 DR PROSITE; PS00948; PAN; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR Blood coagulation; Direct protein sequencing; Fibrinolysis; Hydrolase;
 KW Kringle; Protease; Repeat; Serine protease; Signal; Tissue remodeling;
 KW Zymogen.
 FT SIGNAL 1 19
 FT CHAIN 20 812 Plasminogen.
 FT /FTid=PRO_0000028069.
 FT Plasmin heavy chain A.
 FT CHAIN 20 581 /FTid=PRO_0000028070.
 FT Activation peptide.
 FT PEPTIDE 20 97 /FTid=PRO_0000028071.
 FT Plasmin heavy chain A, short form.
 FT CHAIN 98 581 /FTid=PRO_0000028072.
 FT Angiotensin.
 FT CHAIN 98 7436 /FTid=PRO_0000028073.
 FT Plasmin light chain B.
 FT CHAIN 582 812 /FTid=PRO_0000028074.
 FT PAN.
 FT DOMAIN 20 98
 FT Kringle 1.
 FT DOMAIN 103 181
 FT Kringle 2.
 FT DOMAIN 184 262
 FT Kringle 3.
 FT DOMAIN 275 352
 FT Kringle 4.
 FT DOMAIN 377 454
 FT Kringle 5.
 FT DOMAIN 481 560
 FT Peptidase S1.
 FT DOMAIN 582 810
 FT Charge relay system (By similarity).
 FT ACT_SITE 624 624
 FT Charge relay system (By similarity).
 FT ACT_SITE 667 667
 FT Charge relay system (By similarity).
 FT ACT_SITE 762 762
 FT By similarity.
 FT DISULFID 49 73
 FT By similarity.
 FT DISULFID 53 61
 FT By similarity.
 FT DISULFID 103 181
 FT By similarity.
 FT DISULFID 124 164
 FT By similarity.
 FT DISULFID 152 176
 FT By similarity.
 FT DISULFID 185 262
 FT By similarity.
 FT DISULFID 198 316
 FT By similarity.
 FT DISULFID 206 245
 FT By similarity.
 FT DISULFID 234 257
 FT By similarity.
 FT DISULFID 275 352
 FT By similarity.
 FT DISULFID 296 335
 FT By similarity.
 FT DISULFID 324 347
 FT By similarity.

FT DISULFID 377 454 By similarity.
 FT DISULFID 398 437 By similarity.
 FT DISULFID 426 449 By similarity.
 FT DISULFID 481 560 By similarity.
 FT DISULFID 502 543 By similarity.
 FT DISULFID 531 555 By similarity.
 FT DISULFID 568 687 Interchain (between A and B chains) (By similarity).
 FT DISULFID 578 586 Interchain (between A and B chains) (By similarity).
 Query Match 83.1%; Score 1279; DB 1; Length 812;
 Best Local Similarity 81.0%; Pred. No. 2e-89;
 Matches 209; Conservative 22; Mismatches 27; Indels 0; Gaps 0;
 QY 1 VYLSECKTGNGKVRGTMKNGITCKWSTSRPRFSPATHPSSELEENYCRNPON 60
 DB 98 VYLSECKTGNGYRGTSRTKSGVACQKMGATFPHVFNYSPTHPNELEENYCRNPON 157
 QY 61 DPQGPWCYTTDPKRYDYCDILLECEECWHGSGENYDGRKISKTMSGLECQAWDSQSPHAH 120
 DB 158 DEQGPWCYTTDPKRYDYCNIPCECEECWYCSGKYEKISKTMSGLDQAWDSQSPHAH 217
 QY 121 GYIPSKFPNKLKKYCNRPDRELPRWCFTTDPNKRWELCDIPRCTTPPPSSGPTVQCLK 180
 DB 218 GYIPAKFPNKLKKYCNRPDCEPRWCFTTDPNKRWELCDIPRCTTPPPSSPTVQCLK 277
 QY 181 GTGENYGNVAVTWSGHTCOHWSAOTPHTHERTPENFCCKLDENYCRNPDGKRAPWCHT 240
 DB 278 GRGENYGTVSVTSGKTCQRMSEQTPHRHNNTPENFCCKLEENYCRNPDGETAPWCYT 337
 QY 241 TNSQVRWEYCKIPSCDSS 258
 DB 338 TDSQLRWEYCEIPSCSS 355
 RESULT 12
 Q3VIT9 MOUSE
 ID Q3VIT9 MOUSE PRELIMINARY; PRT; 812 AA.
 AC Q3VIT9
 DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.
 DT 11-OCT-2005, sequence version 1.
 DT 07-FEB-2006, entry version 6.
 DE 18 days pregnant adult female placenta and extra embryonic tissue
 DE cDNA, RIKEN full-length enriched library, clone:3830402P08
 DE product:Plasminogen, full insert sequence.
 GN Name=PIg;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Placenta and extra embryonic tissue;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Methods Enzymol. 303:19-44(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Placenta and extra embryonic tissue;
 RX PubMed=16141072; DOI=10.1126/science.1112014;
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
 Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
 Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Allen J.E.,
 Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
 Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
 Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
 Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
 Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
 di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
 Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
 Georgii-Heminger P., Gingeras T.R., Gojobori T., Green R.E.,

RA Gustinich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N., Hill D., Humineck L., Iacono M., Ikeo K., Iwana A., Ishikawa T., Jakt M., Kanapin A., Katon M., Kawasawa Y., Kelson J., Kitamura H., Kitanoh H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K., Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J., Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L., Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K., Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P., Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O., Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Pesole G., Petrovsky N., Piazza S., Reid J., Reid J.F., Ring B.Z., Ringwald M., Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C., Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y., Shibata Y., Shimada H., Shinada K., Silva D., Sinclair B., Sperling S., Supta E., Sugiyura K., Sultana R., Takenaka Y., Taki K., Tanno H.K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A., Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K., Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C., Grimmond S.M., Teasdale R.D., Liu B.T., Brusic V., Quackenbush J., Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y., Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T., Iida J., Inamura K., Itoh M., Kato T., Kawaji H., Kawagashira N., Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N., Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S., Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J., Hayashizaki Y.

RT "The transcriptional landscape of the mammalian genome.";
 RL Science 309:1559-1563 (2005).

RL [3]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Placenta and extra embryonic tissue;
 RX PubMed16141073; DOI=10.1126/science.1112009;

RG RIKEN Genome Exploration Research Group, and Genome Science Group (Genome Network Core Team) and the FANTOM Consortium;

RG "Antisense Transcription in the Mammalian Transcriptome.";
 RL Science 309:1564-1566 (2005).

RL [4]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Placenta and extra embryonic tissue;
 RX MEDLINE=22354683; PubMed12469851; DOI=10.1038/nature01266;

RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S., Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W., Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S., Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J., Grimmond S., Gustinich S., Hirokawa N., Jackson I.J., Jarvis E.D., Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L., Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H., Nagashima T., Numata K., Okido T., Pavan W.J., Perlea G., Pesole G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S., Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C., Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L., Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K., Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.

RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
 RL Nature 420:563-573 (2002).

RL [5]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Placenta and extra embryonic tissue;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S., Hayashizaki Y.

RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690 (2001).

RL [6]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Placenta and extra embryonic tissue;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;

RA Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.

RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630 (2000).

RL [7]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Placenta and extra embryonic tissue;
 RX MEDLINE=2030913; PubMed=11076861; DOI=10.1101/gr.152600;

RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.

RT "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771 (2000).

RL [8]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Placenta and extra embryonic tissue;
 RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K., Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S., Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N., Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D., Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A., Muramatsu M., Hayashizaki Y.

RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.

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CC -----

CC EMBL; AK132254; BAE21060.1; -; mRNA.

DR MGI; MGI:97620; Plg.

DR GO; GO:0005576; C:extracellular region; RCA.

DR GO; GO:0003179; F:hormone activity; RCA.

DR GO; GO:0006915; P:apoptosis; IDA.

DR GO; GO:0006917; P:induction of apoptosis; IDA.

DR GO; GO:0046716; P:muscle maintenance; IMP.

DR GO; GO:0045445; P:myoblast differentiation; IMP.

DR GO; GO:0016525; P:negative regulation of angiogenesis; TAS.

DR GO; GO:0042246; P:tissue regeneration; IMP.

DR InterPro; IPR000001; Kringle.

DR InterPro; IPR003014; PAN.

DR InterPro; IPR003609; Pan app.

DR InterPro; IPR011358; Pept SIA plasmin.

DR InterPro; IPR001254; Peptidase S1 S6.

DR InterPro; IPR001314; Peptidase_S1A.

DR InterPro; IPR003966; Peptidase_S1A_pp.

DR Pfam; PF00051; Kringle; 5.

DR Pfam; PF00024; PAN_1; 1.

DR Pfam; PF00089; Trypsin; 1.

DR PIRSF; PIRSF001150; Plasmin; 1.

DR PRINTS; PRO0722; CHYMOTRYPSIN.

DR PRINTS; PRO0018; KRINGLE.

DR PRINTS; PRO1505; PROTHROMBIN.

DR ProDom; PD000395; Kringle; 5.

DR SMART; SM00130; KR; 5.

DR SMART; SM00473; PAN_AP; 1.

DR SMART; SM00020; TRYPSIN; 1.

DR PROSITE; PS00021; KRINGLE_1; 5.

DR PROSITE; PS00070; KRINGLE_2; 5.

DR PROSITE; PS00948; PAN; 1.

DR PROSITE; PS0240; TRYPSIN_DOM; 1.

DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.

DR PROSITE; PS00135; TRYPSIN_SER; 1.

Query Match

Best Local Similarity 83.1%; Score 1279; DB 2; Length 812;

Matches 209; Conservative 22; Mismatches 27; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGNYRGTMSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN 60

DB 98 VYLSECKTGNGNYRGTMSRTKSGVACQKMGATPHVPNYSPTHEGLEENYCRNPDN 157

QY 61 DQGPWCYTTDEKRYDYDCIILECEBECMHCSENGYDGIKSTMGLECAQWDSQSPHAX 120

DB 158 DRQGPWCYTTDPKRYDYDCNIPECEBECMYCSEKYEKISKSTMGSLDCAQWDSQSPHAX 217

QY 121 GYIPSPKPNKLKKNYCRNPDELPRWCFTTDPNKRWELCDIPRCTTTPPSGPTVQCULK 180

DB 218 GYIPAKFPKPNKLKKNYCRNPDELPRWCFTTDPNKRWELCDIPRCTTTPPSGPTVQCULK 277

QY 181 GTGNYRGNAVTVSGHTCQHSQAQTPHTERTPENFPCKNLNDENYCRNPDGKRAPWCHT 240

DB 278 GRGNYRGVTVSGTKTCQHSQAQTPHTERTPENFPCKNLNDENYCRNPDGKRAPWCHT 337

QY 241 TNSQVREYCKIPSCDSS 258

DB 338 TDSQVREYCKIPSCSS 355

RESULT 13

ID PLMN ERIEU

AC Q29485; STANDARD; PRT; 810 AA.

DT 01-NOV-1997, integrated into UniProtKB/Swiss-Prot.

DT 01-NOV-1997, sequence version 1.

DE 07-WAR-2006, entry version 52.

DE Plasminogen precursor (EC 3.4.21.7) [Contains: Plasmin heavy chain A;

DE Activation peptide; Plasmin heavy chain A, short form; Plasmin light

DE chain B].

GN Name=PLG;

OS Eriaceae europaeus (Western European hedgehog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Laurasiatheria; Insectivora; Erinaceidae;

OC Erinaceinae; Erinaceus.

OX NCBI_TaxID=9365;

RN [1]_TaxID=9365;

RP NUCLEOTIDE SEQUENCE [MRNA].

RC TISSUE=Liver;

RX MEDLINE=96025778; PubMed=7592597; DOI=10.1074/jbc.270.41.24004;

RA Lawn R.M., Boonmark N.W., Schwartz K., Lindahl G.E., Wade D.P.,

RA Byrne C.D., Fong K.J., Meer K., Patthy L.

RT "The recurring evolution of lipoprotein(a). Insights from cloning of

RT hedgehog apolipoprotein(a).";

RL J. Biol. Chem. 270:24004-24009(1995).

RN [2]

RN SEQUENCE REVISION.

RA Lawn R.M.;

RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.

-!- FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as a proteolytic factor in a variety of other processes including embryonic development, tissue remodeling, tumor invasion, and inflammation; in ovulation it weakens the walls of the Graafian follicle. It activates the urokinase-type plasminogen activator, collagenases and several complement zymogens, such as C1 and C5. It cleaves fibrin, fibronectin, thrombospondin, laminin and von Willebrand factor. Its role in tissue remodeling and tumor invasion may be modulated by CSPG4.

-!- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa; higher selectivity than trypsin. Converts fibrin into soluble products.

-!- ENZYME REGULATION: Converted into plasmin by plasminogen activators, both plasminogen and its activator being bound to fibrin. Cannot be activated with streptokinase.

-!- SUBUNIT: Interacts with CSPG4 (By similarity).

-!- SUBCELLULAR LOCATION: Secreted protein.

-!- DOMAIN: Kringle domains mediate interaction with CSPG4 (By similarity).

-!- PTM: In the presence of the inhibitor, the activation involves only cleavage after Arg-582, yielding two chains held together by two disulfide bonds. In the absence of the inhibitor, the activation involves additionally the removal of the activation peptide (By similarity).

-!- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin immediately after dissociation from the clot.

-!- SIMILARITY: Belongs to the peptidase S1 family. Plasminogen subfamily.

-!- SIMILARITY: Contains 5 kringle domains.

-!- SIMILARITY: Contains 1 PAN domain.

-!- SIMILARITY: Contains 1 peptidase S1 domain.

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EMBL; U33171; AAC48717.1; -; mRNA.

PIR; I46260; I46260.

HSSP; P00747; 1BUI.

SMR; Q29485; 568-810.

MEROPS; S01.233; -.

InterPro; IPR000001; Kringle.

InterPro; IPR003014; PAN.

InterPro; IPR003609; Pan_app.

InterPro; IPR011358; Pept_S1A_plasmin.

InterPro; IPR001254; Peptidase_S1_S6.

InterPro; IPR001314; Peptidase_S1A.

InterPro; IPR003966; Peptidase_S1A_pp.

Pfam; PF00051; Kringle; 5.

Pfam; PF00024; PAN_1; 1.

Pfam; PF00089; Trypsin; 1.

PIRSF; PIRSF001150; Plasmin; 1.

PRINTS; PRO0722; CHYMOTRYPSIN.

PRINTS; PRO0018; KRINGLE.

PRINTS; PRO1505; PROTHROMBIN.

ProDom; PD000395; Kringle; 5.

SMART; SM00130; KR; 5.

SMART; SM00473; PAN_AP; 1.

SMART; SM00020; Tryp_Spc; 1.

PROSITE; PS00021; KRINGLE_1; 5.

PROSITE; PS00070; KRINGLE_2; 5.

PROSITE; PS00948; PAN; 1.

PROSITE; PS0240; TRYPSIN_DOM; 1.

PROSITE; PS00134; TRYPSIN_HIS; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.

KW Blood coagulation; Fibrinolysis; Glycoprotein; Hydrolase; Kringle;

KW Protease; Repeat; Serine protease; Signal; Tissue remodeling; Zymogen.

SIGNAL 1 19 By similarity.

CHAIN 20 810 Plasminogen.

/FTID=PRO_0000028046.

FT CHAIN 20 582 Plasmin heavy chain A (By similarity).

FT /FTID=PRO_0000028047.

FT PEPTIDE 20 97 Activation peptide (By similarity).

FT /FTID=PRO_0000028048.

```

FT CHAIN 98 582 Plasmin heavy chain A, short form (By
FT similarity).
FT /FTID=PRO_0000028049.
FT CHAIN 583 810 Plasmin light chain B (By similarity).
FT /FTID=PRO_0000028050.
FT PAN.
FT DOMAIN 20 98 Kringle 1.
FT DOMAIN 103 181 Kringle 2.
FT DOMAIN 185 262 Kringle 3.
FT DOMAIN 275 352 Kringle 4.
FT DOMAIN 379 456 Kringle 5.
FT DOMAIN 482 561 Peptidase S1.
FT DOMAIN 582 808 Charge relay system.
FT ACT_SITE 622 622 Charge relay system.
FT ACT_SITE 665 665 Charge relay system.
FT ACT_SITE 760 760 Charge relay system.
FT CARBOHYD 339 339 N-linked (GlcNAc...) (Potential).
FT DISULFID 49 73 By similarity.
FT DISULFID 53 61 By similarity.
FT DISULFID 103 181 By similarity.
FT DISULFID 124 164 By similarity.
FT DISULFID 152 176 By similarity.
FT DISULFID 185 262 By similarity.
FT DISULFID 188 316 By similarity.
FT DISULFID 206 245 By similarity.
FT DISULFID 234 257 By similarity.
FT DISULFID 275 352 By similarity.
FT DISULFID 296 335 By similarity.
FT DISULFID 324 347 By similarity.
FT DISULFID 379 456 By similarity.
FT DISULFID 400 439 By similarity.
FT DISULFID 428 451 By similarity.
FT DISULFID 482 561 By similarity.
FT DISULFID 503 544 By similarity.
FT DISULFID 532 556 By similarity.
FT DISULFID 569 685 Interchain (between A and B chains) (By
FT similarity).
FT DISULFID 579 586 Interchain (between A and B chains) (By
FT similarity).
FT DISULFID 607 623 By similarity.
FT DISULFID 699 766 By similarity.
FT DISULFID 729 745 By similarity.
FT DISULFID 756 784 By similarity.
FT SEQUENCE 810 AA; 90902 MW; 8E75780946017A16 CRC64;
Query Match 80.3%; Score 1237; DB 1; Length 810;
Best Local Similarity 77.9%; Pred. No. 3.2e-86;
Matches 201; Conservative 26; Mismatches 31; Indels 0; Gaps 0;
QY 1 VYLSECKTGNKNGYRTMSKTKNGITCQKWSSTSPHRPRSPATHPSEGLEENYCRNPDN 60
DB 98 MYLSECKVGNKYRTGTVSKTKTGLTCQKWSAETHPKRPSDENPSEGLDQNYCRNPDN 157
QY 61 DPGPWCYTTDPKRYDYCDILECEBECMHCSENYDGKISKTMGLCQAWDSQSPHAH 120
DB 158 DPGPWCYTTDPKRYDYCDILECEBECMHCSENYDGKISKTMGLCQAWDSQSPHAH 217
QY 121 GYIPSKFPNKLKKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTPPPSSGPTYQCLK 180
DB 218 GYIPSKFPNKLKKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTPPPSSGPTYQCLM 277
QY 181 GYGNTRGNVAVTVSGHTCOHWSAQTPHTERTPENFPCKNLNDENYCRNPDGKRAPWCHT 240
DB 278 GNGEYQGNVAVTVSGTLCQRWGEQSPHRHRTPEYPCNKLNDENYCRNPDGSPAPWCFT 337
QY 241 TNSQVREYCKIPSCDSS 258
DB 338 TNSSVREYCKIPDCVSS 355

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RESULT 14

Q7TP84_RAT

ID: Q7TP84_RAT

AC Q7TP84;

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DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2003, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE Ab1-346.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Xu C.S., Li W.Q., Li Y.C., Yan H.M., Chang C.P., Zhao L.F., Ma H.,
RA Wang L., Wang S.F., Han H.P., Wang G.P., Chai L.O., Yuan J.Y.,
RA Yang K.J., Shi J.B., Rahman S., Wang Q.N., Zhang J.B.,
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
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EMBL: AV325159; AAP92560.1; -; mRNA.
DR HSSP; P00747; IBI.
DR SMR; Q7TP84; 83-360, 661-759.
DR Ensembl; ENSRNOG0000017223; Rattus norvegicus.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004283; F:plasmin activity; IEA.
DR GO; GO:0007596; P:blood coagulation; IEA.
DR GO; GO:0050874; P:organismal physiological process; IEA.
DR GO; GO:0006508; P:proteolysis; IEA.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR003014; PAN.
DR InterPro; IPR011358; Pept_SIA_Plasmin.
DR InterPro; IPR001254; Peptidase_S1_S6.
DR InterPro; IPR003966; Peptidase_S1A_pp.
DR Pfam; PF00051; Kringle; 5.
DR Pfam; PF00024; PAN 1; 1.
DR Pfam; PF00089; Trypsin; 2.
DR PIRSF; PIRSF001150; Plasmin; 1.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR01505; PROTHROMBIN.
DR ProDom; PD000395; Kringle; 5.
DR SMART; SM00130; KR; 5.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00021; KRINGLE_1; 5.
DR PROSITE; PS00070; KRINGLE_2; 5.
DR PROSITE; PS02440; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN 1.
DR SEQUENCE 759 AA; 86057 MW; 1422BFAC05C6DFA7 CRC64;
Query Match 78.1%; Score 1203.5; DB 2; Length 759;
Best Local Similarity 71.1%; Pred. No. 1.1e-93;
Matches 204; Conservative 22; Mismatches 28; Indels 33; Gaps 2;
QY 1 VYLSECKTGNKNGYRTMSKTKNGITCQKWSSTSPHRPRSPATHPSEGLEENYCRNPDN 60
DB 81 VYLSECKTGNKNGYRTMSKTKNGITCQKWSSTSPHRPRSPATHPSEGLEENYCRNPDN 140
QY 61 DPGPWCYTTDPKRYDYCDILECEBECMHCSENYDGKISKTMGLCQAWDSQSPHAH 120
DB 141 DPGPWCYTTDPKRYDYCDILECEBECMHCSENYDGKISKTMGLCQAWDSQSPHAH 200
QY 121 GYIPSKFPNKLKKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTPPPSSGPTYQCLM 166
DB 201 GYIPAKFPNKLKKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTPPPSSGPTYQCLM 260
QY 167 -----TPPPSSGPTYQCLMTPNKRWELCDIPRCTTPPPSSGPTYQCLM 211
DB 261 IFIIFIIFIIFIIFIIFIIFIIFIIFIIFIIFIIFIIFIIFIIFIIFIIFIIFIIFIIFI 316
QY 212 RTPENFPCKNLNDENYCRNPDGKRAPWCHTTPNKRWELCDIPRCTTPPPSSGPTYQCLM 258
DB 317 RTPENFPCKNLNDENYCRNPDGKRAPWCHTTPNKRWELCDIPRCTTPPPSSGPTYQCLM 363

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RES: 15
 PLMN MACEU
 ID PLMN MACEU STANDARD; PRT; 806 AA.
 AC 018783;
 DT 31-AUG-2004, integrated into UniProtKB/Swiss-Prot.
 DT 01-JAN-1998, sequence version 1.
 DT 07-MAR-2006, entry version 40.
 DE Plasminogen precursor (EC 3.4.21.7) [Contains: Plasmin heavy chain A;
 DE Activation peptide; Plasmin heavy chain A, short form; Plasmin light
 DE chain B].
 GN Name=PLG;
 OS Macropus eugenii (Tamar wallaby).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
 OX NCBI_TaxID=9315;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RC TISSUE=Liver;
 RX MEDLINE=98004511; PubMed=9342350; DOI=10.1073/pnas.94.22.11992;
 RA Lawn R.M., Schwartz K., Patchy L.;
 RT "Convergent evolution of apolipoprotein(a) in primates and hedgehog.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:11992-11997(1997).
 CC -!- FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as
 CC a proteolytic factor in a variety of other processes including
 CC embryonic development, tissue remodeling, tumor invasion, and
 CC inflammation; in ovulation it weakens the walls of the Graafian
 CC follicle. It activates the urokinase-type plasminogen activator,
 CC collagenases and several complement zymogens, such as C1 and C5.
 CC It cleaves fibrin, fibronectin, thrombospondin, laminin and von
 CC Willebrand factor. Its role in tissue remodeling and tumor
 CC invasion may be modulated by CSPG4 (By similarity).
 CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Lys-[Xaa > Arg]-Xaa;
 CC higher selectivity than trypsin. Converts fibrin into soluble
 CC products.
 CC -!- ENZYME REGULATION: Converted into plasmin by plasminogen
 CC activators, both plasminogen and its activator being bound to
 CC fibrin. Activated with catalytic amounts of streptokinase (By
 CC similarity).
 CC -!- SUBUNIT: Interacts with CSPG4 (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted protein.
 CC -!- DOMAIN: Kringle domains mediate interaction with CSPG4 (By
 CC similarity).
 CC -!- PTM: In the presence of the inhibitor, the activation involves
 CC only cleavage after Arg-576, yielding two chains held together by
 CC two disulfide bonds. In the absence of the inhibitor, the
 CC activation involves additionally the removal of the activation
 CC peptide (By similarity).
 CC -!- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin
 CC immediately after dissociation from the clot (By similarity).
 CC -!- MISCELLANEOUS: In the presence of the inhibitor, the activation
 CC involves only cleavage after Arg-576, resulting in 2 chains held
 CC together by 2 disulfide bonds. Without the inhibitor, the
 CC activation involves also removal of the activation peptide (By
 CC similarity).
 CC -!- SIMILARITY: Belongs to the peptidase S1 family. Plasminogen
 CC subfamily.
 CC -!- SIMILARITY: Contains 5 kringle domains.
 CC -!- SIMILARITY: Contains 1 PAN domain.
 CC -!- SIMILARITY: Contains 1 peptidase S1 domain.
 CC -----
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 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL: AF012297; AAB65760.1; -; mRNA.
 DR HSSP: P00747; 1BUT.
 DR SMR: O18783; 561-806.
 DR MEROPS: S01.233; -.
 DR InterPro: IPR000001; Kringle.
 DR InterPro: IPR003014; PAN.
 DR InterPro: IPR003609; Pan_app.
 DR InterPro: IPR011358; Pept_S1A_Plasmin.
 DR InterPro: IPR001254; Peptidase_S1_S6.
 DR InterPro: IPR001314; Peptidase_S1A.

DR InterPro: IPR003966; Peptidase_S1A_pp.
 DR Pfam: PF00051; Kringle; 5.
 DR Pfam: PF00024; PAN_1; 1.
 DR Pfam: PF00089; Trypsin; 1.
 DR FIRSF: FIRSF001150; Plasmin; 1.
 DR PRINTS: PRO0722; CHYMOTRYPSIN.
 DR PRINTS: PRO0018; KRINGLE.
 DR PRINTS: PRO1505; PROTHROMBIN.
 DR ProDom: PD000395; Kringle; 5.
 DR SMART: SM00130; KR; 5.
 DR SMART: SM00473; PAN AP; 1.
 DR SMART: SM00020; Tryp_SPC; 1.
 DR PROSITE: PS00021; KRINGLE_1; 5.
 DR PROSITE: PS00070; KRINGLE_2; 5.
 DR PROSITE: PS50948; PAN; 1.
 DR PROSITE: PS50240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; 1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 DR Blood coagulation; Fibrinolysis; Hydrolase; Kringle; Repeat;
 KW Serine protease; Signal; Tissue remodeling; Zymogen.
 FT SIGNAL 1 19 Potential.
 FT CHAIN 20 806 Plasminogen.
 FT /FTID=PRO_0000028064. Plasmin heavy chain A (By similarity).
 FT CHAIN 20 576 /FTID=PRO_0000028065. Activation peptide (By similarity).
 FT PEPTIDE 20 96 /FTID=PRO_0000028066. Plasmin heavy chain A, short form (By
 FT CHAIN 97 576 similarity).
 FT /FTID=PRO_0000028067. Plasmin light chain B (By similarity).
 FT CHAIN 577 806 /FTID=PRO_0000028068.
 FT DOMAIN 20 98 PAN.
 FT DOMAIN 102 181 Kringle 1.
 FT DOMAIN 184 262 Kringle 2.
 FT DOMAIN 274 352 Kringle 3.
 FT DOMAIN 370 448 Kringle 4.
 FT DOMAIN 475 555 Kringle 5.
 FT DOMAIN 577 804 Peptidase S1.
 FT ACT_SITE 618 618 Charge relay system (By similarity).
 FT ACT_SITE 661 661 Charge relay system (By similarity).
 FT ACT_SITE 756 756 Charge relay system (By similarity).
 FT DISULFID 49 73 By similarity.
 FT DISULFID 53 61 By similarity.
 FT DISULFID 103 181 By similarity.
 FT DISULFID 124 164 By similarity.
 FT DISULFID 152 176 By similarity.
 FT DISULFID 185 262 By similarity.
 FT DISULFID 188 316 By similarity.
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 FT DISULFID 392 431 By similarity.
 FT DISULFID 420 443 By similarity.
 FT DISULFID 476 555 By similarity.
 FT DISULFID 497 538 By similarity.
 FT DISULFID 526 550 By similarity.
 FT DISULFID 563 681 Interchain (between A and B chains) (By
 FT DISULFID 573 581 similarity).
 FT DISULFID 573 581 Interchain (between A and B chains) (By
 FT DISULFID 603 619 similarity).
 FT DISULFID 695 762 By similarity.
 FT DISULFID 725 741 By similarity.
 FT DISULFID 752 780 By similarity.
 SQ SEQUENCE 806 AA; 90981 MW; 95FAA86DC20064D5 CRC64;

Query Match 75.3%; Score 1160; DB 1; Length 806;
 Best Local Similarity 71.7%; Pred. No. 2.5e-80;
 Matches 185; Conservative 34; Mismatches 39; Indels 0; Gaps 0;

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 29, 2006, 13:56:28 ; Search time 39 Seconds
(without alignments)
641.445 Million cell updates/sec

Title: US-09-502-176-2

Perfect score: 1540

Sequence: 1 VYLSCKTGNGKNGYRTWSK.....TNSQVRWEYCKIPDCSSPV 260

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 80:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1535	99.7	810	1 PLHU	plasmin (EC 3.4.21)
2	1442	93.6	810	2 B30848	plasmin (EC 3.4.21)
3	1292	83.9	790	1 PLPG	plasmin (EC 3.4.21)
4	1291	83.8	812	1 PLBO	plasmin (EC 3.4.21)
5	1274	82.7	812	1 PLMS	plasmin (EC 3.4.21)
6	1237	80.3	810	2 I46260	plasmin (EC 3.4.21)
7	881	57.2	2869	2 T18518	apolipoprotein(a)
8	797	51.8	728	1 JH0579	hepatocyte growth
9	782	50.8	728	1 A35644	hepatocyte growth
10	776.5	50.4	710	1 I51283	hepatocyte growth
11	776	50.4	728	1 A60185	hepatocyte growth
12	766.5	49.8	716	1 JCS061	macrophage-stimula
13	754.5	48.9	411	2 I51285	hepatocyte growth
14	753.5	48.9	716	1 A40332	macrophage-stimula
15	749	48.6	4548	1 S00657	apoprotein(a) (EC
16	739	48.0	711	1 A47136	macrophage-stimula
17	739	48.0	1420	2 A32869	apolipoprotein(a)
18	505	32.8	455	2 A61545	plasmin (EC 3.4.21)
19	499	32.4	460	2 B61545	plasmin (EC 3.4.21)
20	391.5	25.4	336	2 S33879	plasmin precursor
21	372	24.2	625	1 TBBO	thrombin (EC 3.4.2
22	362.5	23.5	169	2 A40522	plasmin (EC 3.4.21
23	357.5	23.2	618	2 A35627	thrombin (EC 3.4.2
24	351	22.8	622	1 TBHU	thrombin (EC 3.4.2
25	348	22.6	617	2 S10511	thrombin (EC 3.4.2
26	309.5	20.1	562	1 UKHUT	t-plasminogen acti
27	265.5	19.2	559	1 A35029	t-plasminogen acti
28	281.5	18.3	559	1 A29941	t-plasminogen acti
29	278	18.1	120	2 E61545	plasmin (EC 3.4.21

30	271	17.6	89	2 A60140	plasmin (EC 3.4.21
31	268	17.4	123	2 C61545	plasmin (EC 3.4.21
32	241.5	15.7	937	2 A45082	neurotrophic recep
33	240	15.6	943	2 B45082	neurotrophic recep
34	237.5	15.4	946	1 A47299	ror-related recept
35	233	15.1	603	2 S28941	coagulation factor
36	214	13.9	558	2 JCS878	plasma hyaluronan-
37	210	13.6	560	1 JCA795	plasma hyaluronan-
38	201	13.1	291	2 I38098	t-plasminogen acti
39	198	12.9	615	1 KFHU12	coagulation factor
40	190.5	12.4	593	2 S45281	coagulation factor
41	188.5	12.2	655	1 A46688	hepatocyte growth
42	178.5	11.6	806	2 T18840	hypothetical prote
43	165	10.7	433	1 JN0560	u-plasminogen acti
44	153	9.9	442	1 UKPG	u-plasminogen acti
45	151	9.8	432	1 S18932	u-plasminogen acti

ALIGNMENTS

RESULT 1

PLHU

plasmin (EC 3.4.21.7) precursor [validated] - human

N:Alternate names: plasminogen precursor [misnomer]

N:Contains: angiotensin; microplasmin; plasminogen

C:Species: Homo sapiens (man)

C>Date: 24-Apr-1984 #sequence revision 02-Dec-1994 #text change 09-Jul-2004

C:Accession: A35229; I52242; A26646; I62738; I84609; S03735; A00929; A04627; A04625; A046

R:Petersen, T.E.; Martzen, M.R.; Ichinose, A.; Davie, E.W.

J. Biol. Chem. 265, 6104-6111, 1990

A:Title: Characterization of the gene for human plasminogen, a key proenzyme in the fibrin

A:Reference number: A35229; MUID:90202879; PMID:2318848

A:Accession: A35229

A:Molecule type: DNA

A:Residues: 1-810 <PEP>

A:Cross-references: UNIPROT:P00747; UNIPROT:Q9UBQ9; UNIPROT:Q9UMI2; UNIPARC:UPI0000016AEC

A:Experimental source: leukocyte; lung fibroblast

R:Malgarutti, N.; Bruno, L.; Pontoglio, M.; Candiani, G.; Meroni, G.; Ottolenghi, S.; Tar

Biochem. Biophys. Res. Commun. 173, 1013-1018, 1990

A:Title: Definition of the transcription initiation site of human plasminogen gene in liv

A:Reference number: I52242; MUID:91097523; PMID:2568308

A:Accession: I52242

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-16 <MAL1>

A:Cross-references: UNIPARC:UPI0000062A8; GB:M62890; NID:G190092; PIDN:AAA36454.1; PID:5

R:Forsgren, M.; Raden, B.; Israelsson, M.; Larsson, K.; Heden, L.O.

FEBS Lett. 213, 254-260, 1987

A:Title: Molecular cloning and characterization of a full-length cDNA clone for human pla

A:Reference number: A26646; MUID:87162490; PMID:3030813

A:Accession: A26646

A:Molecule type: mRNA

A:Residues: 1-471, 'D', 473-810 <FOR>

A:Cross-references: UNIPARC:UPI000000DBB8; GB:X05199; NID:G35530; PIDN:CRA28831.1; PID:G

A:Experimental source: liver

R:Malinowski, D.P.; Sadler, J.E.; Davie, E.W.

Biochemistry 23, 4243-4250, 1984

A:Title: Characterization of a complementary deoxyribonucleic acid coding for human and t

A:Reference number: I45961; MUID:85023311; PMID:6148961

A:Accession: I62738

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 292-471, 'D', 473-810 <MAL2>

A:Cross-references: UNIPARC:UPI000016AED4; GB:K02922; NID:G190112; PIDN:AAA60124.1; PID:5

A:Accession: I84609

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 367-419 <MAL3>

A:Cross-references: UNIPARC:UPI0000071C7D; GB:K02921; NID:G190110; PIDN:AAA60123.1; PID:5

R:Brinsholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Manneberg, M.;

Eur. J. Biochem. 114, 465-470, 1981

A:Title: Comparison of the primary structure of the N-terminal CNBr fragments of human, t

A;Reference number: A51488; PDB:2PK4
A;Contents: annotation; X-ray crystallography, 2.25 angstroms, residues 375-454
R;Wu, T.P.; Tulinsky, A.
submitted to the Brookhaven Protein Data Bank, August 1993
A;Reference number: A51911; PDB:1PKR
A;Contents: annotation; X-ray crystallography, 2.48 angstroms, residues 102-181
R;Padmanabhan, K.; Tulinsky, A.
submitted to the Brookhaven Protein Data Bank, April 1994
A;Reference number: A52408; PDB:1PMK
A;Contents: annotation; X-ray crystallography, 2.25 angstroms, residues 377-454
R;Tulinsky, A.; Mathews, I.I.
submitted to the Brookhaven Protein Data Bank, December 1995
A;Reference number: A65244; PDB:1CEA
A;Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 102-181
R;Tulinsky, A.; Mathews, I.I.
submitted to the Brookhaven Protein Data Bank, December 1995
A;Reference number: A65245; PDB:1CEB
A;Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 102-181
R;Mulichak, A.M.; Tulinsky, A.; Ravichandran, K.G.
Biochemistry 30, 10576-10588, 1991
A;Title: Crystal and molecular structure of human plasminogen kringle 4 refined at 1.9 Å
A;Reference number: A58819; MUID:92031502; PMID:1657148
A;Contents: annotation
R;de Vos, A.M.; Ultsch, M.H.; Kelley, R.P.; Padmanabhan, K.; Tulinsky, A.; Mulichak, A.M.
Biochemistry 30, 10589-10594, 1991
A;Title: The refined structure of the epsilon-aminocaproic acid complex of human plasminogen
A;Reference number: A58818; MUID:92031503; PMID:1657149
A;Contents: annotation
R;de Vos, A.M.; Ultsch, M.H.; Kelley, R.P.; Padmanabhan, K.; Tulinsky, A.; Westbrock, M.I.
Biochemistry 31, 270-279, 1992
A;Title: Crystal structure of the kringle 2 domain of tissue plasminogen activator at 2.4 Å
A;Reference number: A39483; MUID:92118803; PMID:1310033
A;Contents: annotation; X-ray crystallography, 2.4 angstroms
R;Stec, B.; Teeter, M.M.; Whitlow, M.; Yamano, A.
submitted to the Brookhaven Protein Data Bank, June 1995
A;Reference number: A65980; PDB:1KKN
A;Contents: annotation; X-ray crystallography, 1.67 angstroms, residues 376-454
R;Rejante, M.; Llinas, M.
submitted to the Brookhaven Protein Data Bank, August 1996
A;Reference number: A65803; PDB:1HPJ
A;Contents: annotation; conformation by (1)H-NMR, residues 103-181
R;Rejante, M.; Llinas, M.
submitted to the Brookhaven Protein Data Bank, August 1996
A;Reference number: A65804; PDB:1HPK
A;Contents: annotation; conformation by (1)H-NMR, residues 103-181
R;Rejante, M.R.; Llinas, M.
Eur. J. Biochem. 221, 927-937, 1994
A;Title: (1)H-NMR assignments and secondary structure of human plasminogen kringle 1.
A;Reference number: A43645; MUID:94237157; PMID:8181475
A;Contents: annotation; conformation by (1)H-NMR, residues 96-184
R;Rejante, M.R.; Llinas, M.
Eur. J. Biochem. 221, 939-949, 1994
A;Title: Solution structure of the epsilon-aminoheptanoic acid complex of human plasminogen
A;Reference number: A58817; MUID:94237158; PMID:8181476
A;Contents: annotation; conformation by (1)H-NMR
C;Comment: Plasminogen is synthesized by the kidney and is present in plasma and many other
C;Comment: Plasminogen is converted to plasmin by plasminogen activators (see PIR:UKHU ar
d PIR:FGHUB).
C;Comment: Plasmin is inactivated by alpha-2-antiplasmin (see PIR:ITHUA2) immediately aft
rg-580, resulting in two chains connected by two disulfide bonds. Without the inhibitor,
C;Comment: Microplasmin is formed by autolytic cleavage of plasmin under artificial condi
C;Comment: Stromelysin 1 (see PIR:KCHUS1) acts on plasminogen to produce angiotensin. Toq
ting solid tumors.
C;Genetics:
A;Gene: GDB:PLG
A;Cross-references: GDB:119498; OMIM:173350
A;Map position: 6q26-6q27
A;Introns: 17/1; 62/2; 98/1; 136/2; 183/1; 223/1; 263/1; 317/2; 366/1; 419/2; 480/1; 529/
C;Function:
A;Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a var
ns the walls of the graafian follicle; also activates the urokinase-type plasminogen acti
A;Pathway: fibrinolysis
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology.

C;Keywords: angiogenesis inhibitor; blood; duplication; fibrinolysis; glycoprotein; hydrolase; plasminogen-related protein precursor homology <PLPH>
 F;1-19/Domain: signal sequence #status predicted <SIG>
 F;20-810/Product: plasminogen #status experimental <PRO>
 F;20-96/Domain: activation peptide #status experimental <APT>
 F;79-466/Product: angiotensin #status experimental <AST>
 F;97-580,581-810/Product: plasmin #status experimental <MAT>
 F;97-580/Domain: plasmin chain A #status experimental <CHA>
 F;103-181/Domain: kringles homology <KR1>

Query Match 99.7%; Score 1535; DB 1; Length 810;
 Best Local Similarity 99.6%; Pred. No. 1.6e-104;
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGKNGKNGRTGKNGITCKQWSSTSPHPRFSPATHPSEGLEENYCRNPDN 60
 DB 98 VYLSECKTGKNGKNGRTGKNGITCKQWSSTSPHPRFSPATHPSEGLEENYCRNPDN 157

QY 61 DQGPWCYTTDEKRYDYCDILECEECMHCSGENDGKISKTMSGLEQAWDSQSPH 217
 DB 158 DQGPWCYTTDEKRYDYCDILECEECMHCSGENDGKISKTMSGLEQAWDSQSPH 217

QY 121 GYIPSKFPNNKLNKYNCRNPDRELPRWCFTTDPNKRWELCDIPRCTTPPPSSGTYQCLK 180
 DB 218 GYIPSKFPNNKLNKYNCRNPDRELPRWCFTTDPNKRWELCDIPRCTTPPPSSGTYQCLK 277

QY 181 GTGNYRGNAVTVSGTCHQWSAQTPHTHPENFPCKNLNDENYCRNPDGKRAPWCHT 240
 DB 278 GTGNYRGNAVTVSGTCHQWSAQTPHTHPENFPCKNLNDENYCRNPDGKRAPWCHT 337

QY 241 TNSQVRWEYCKIPSCDSSPV 260
 DB 338 TNSQVRWEYCKIPSCDSSPV 357

RESULT 2
 B30848
 Plasmin (EC 3.4.21.7) precursor - rhesus macaque
 C;Species: Macaca mulatta (rhesus macaque)
 C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
 C;Accession: B32869; B30848
 R;Tomlinson, J.E.; McLean, J.W.; Lawn, R.M.
 J. Biol. Chem. 264, 5957-5965, 1989
 A;Title: Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of synthesis.
 A;Reference number: A32869; MUID:89174660; PMID:2925643
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-810 <TOM>
 A;Cross-references: UNIPROT:P12545; UNIPARC:UPI0000131COP; CB:J04697; NID:G342272; PIDN:
 C;Superfamily: plasmin; kringles homology; plasminogen-related protein precursor homology
 C;Keywords: fibrinolysis; glycoprotein; hydrolase; kringles; serine proteinase
 F;1-9/Domain: plasminogen-related protein precursor homology <PLPH>
 F;103-181/Domain: signal sequence #status predicted <SIG>
 F;103-181/Domain: kringles homology <KR1>
 F;185-262/Domain: kringles homology <KR2>
 F;275-352/Domain: kringles homology <KR3>
 F;377-454/Domain: kringles homology <KR4>
 F;481-560/Domain: kringles homology <KR5>
 F;581-803/Domain: trypsin homology <TRY>
 F;49-73,53-61,103-181,224-164,152-176,185-262,188-316,206-245,234-257,275-352,296-335,32
 bonds: #status predicted
 F;622,665,760/Active site: His, Asp, Ser #status predicted

Query Match 93.6%; Score 1442; DB 2; Length 810;
 Best Local Similarity 93.1%; Pred. No. 9.4e-98;
 Matches 242; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 1 VYLSECKTGKNGKNGRTGKNGITCKQWSSTSPHPRFSPATHPSEGLEENYCRNPDN 60
 DB 98 VYLSECKTGKNGKNGRTGKNGITCKQWSSTSPHPRFSPATHPSEGLEENYCRNPDN 157

QY 61 DQGPWCYTTDEKRYDYCDILECEECMHCSGENDGKISKTMSGLEQAWDSQSPH 217

DB 158 DQGPWCYTTDEKRYDYCDILECEECMHCSGENDGKISKTMSGLEQAWDSQSPH 217
 QY 121 GYIPSKFPNNKLNKYNCRNPDRELPRWCFTTDPNKRWELCDIPRCTTPPPSSGTYQCLK 180
 DB 218 GYIPSKFPNNKLNKYNCRNPDRELPRWCFTTDPNKRWELCDIPRCTTPPPSSGTYQCLK 277

QY 181 GTGNYRGNAVTVSGTCHQWSAQTPHTHPENFPCKNLNDENYCRNPDGKRAPWCHT 240
 DB 278 GTGNYRGNAVTVSGTCHQWSAQTPHTHPENFPCKNLNDENYCRNPDGKRAPWCHT 337

QY 241 TNSQVRWEYCKIPSCDSSPV 260
 DB 338 TNSQVRWEYCKIPSCDSSPV 357

RESULT 3
 PLPG
 plasmin (EC 3.4.21.7) precursor - pig (fragment)
 N;Alternate names: plasminogen
 N;Contains: miniplasminogen
 C;Species: Sus scrofa domestica (domestic pig)
 C;Date: 07-Sep-1990 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
 C;Accession: S03733; S03737; A25834
 R;Schaller, J.; Marti, T.; Roesseler, S.J.; Kaempfer, U.; Rickli, E.E.
 Fibrinolysis 1, 91-102, 1987
 A;Title: Amino acid sequence of the heavy chain of porcine plasmin. Comparison of the car
 A;Reference number: S03733
 A;Accession: S03733
 A;Molecule type: protein
 A;Residues: 1-560 <SCH>
 A;Cross-references: UNIPROT:P06867; UNIPARC:UPI0000172B90
 R;Brunisholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Manneberg, M.;
 Eur. J. Biochem. 114, 465-470, 1981
 A;Title: Comparison of the primary structure of the N-terminal CNBr fragments of human, i
 A;Reference number: S03735; MUID:81212097; PMID:7238497
 A;Accession: S03737
 A;Molecule type: protein
 A;Residues: 1-57 <BRU>
 A;Cross-references: UNIPARC:UPI0000172B91
 R;Marti, T.; Schaller, J.; Rickli, E.E.
 Eur. J. Biochem. 149, 279-285, 1985
 A;Title: Determination of the complete amino-acid sequence of porcine miniplasminogen.
 A;Reference number: A25834; MUID:85203907; PMID:3946533
 A;Accession: A25834
 A;Molecule type: protein
 A;Residues: 450-790 <MAR>
 A;Cross-references: UNIPARC:UPI0000172B92
 C;Function:
 A;Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a vai
 ns the walls of the graafian follicle; also activates the urokinase-type plasminogen acti
 C;Superfamily: plasmin; kringles homology; plasminogen-related protein precursor homology;
 C;Keywords: fibrinolysis; glycoprotein; hydrolase; kidney; kringles; plasma; serine protei
 F;1-790/Product: plasminogen #status predicted <PRO>
 F;1-77/Domain: plasminogen-related protein precursor homology (fragment) <PLPH>
 F;78-560/Product: activation peptide #status predicted <APT>
 F;78-560/Product: plasmin chain A #status predicted <ACH>
 F;84-162/Domain: kringles homology <KR1>
 F;166-243/Domain: kringles homology <KR2>
 F;256-333/Domain: kringles homology <KR3>
 F;358-435/Domain: kringles homology <KR4>
 F;450-790/Product: miniplasminogen #status experimental <MIN>
 F;461-540/Domain: kringles homology <KR5>
 F;561-790/Product: plasmin chain B #status experimental <BCH>
 F;561-783/Domain: trypsin homology <TRY>
 F;30-54,34-42,84-162,105-145,133-157,166-243,169-297,187-226,215-238,256-333,277-316,305-
 bonds: #status predicted
 F;602,645,740/Active site: His, Asp, Ser #status predicted

Query Match 83.9%; Score 1292; DB 1; Length 790;
 Best Local Similarity 81.4%; Pred. No. 8e-87;
 Matches 210; Conservative 23; Mismatches 25; Indels 0; Gaps 0;

eful in treating solid tumors.

C:Function:

A:Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a variety of tissues; dissolves the walls of the Graafian follicle; also activates the urokinase-type plasminogen activator

A:Pathway: fibrinolysis

C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C:Keywords: angiotensin inhibitor; blood; duplication; fibrinolysis; glycoprotein; hydrolysis

F:1-96/Domain: plasminogen-related protein precursor homology <PLPH>

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-812/Product: plasminogen #status predicted <PRO>

F:20-96/Domain: activation peptide #status predicted <APT>

F:79-466/Product: angiotensin #status predicted <AST>

F:97-581.582-812/Product: plasmin #status predicted <MAT>

F:97-581/Domain: chain A #status predicted <ACH>

F:103-181/Domain: kringle homology <KR1>

F:185-262/Domain: kringle homology <KR2>

F:275-352/Domain: kringle homology <KR3>

F:377-454/Domain: kringle homology <KR4>

F:481-560/Domain: kringle homology <KR5>

F:582-812/Domain: chain B #status predicted <BCH>

F:582-805/Domain: trypsin homology <TRY>

F:49-73,53-61,103-181,124-164,152-176,185-262,188-316,206-245,234-257,275-352,296-335,342-352/Domain: #status predicted

F:78-79/Cleavage site: Glu-Asn (stromelysin 1) #status predicted

F:136-308/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:466-467/Cleavage site: Thr-Val (stromelysin 1) #status predicted

F:581-582/Cleavage site: Arg-Val (plasminogen activator) #status experimental

F:624,667,762/Active site: His, Asp, Ser #status predicted

Query Match 82.7%; Score 1274; DB 1; Length 812;

Best Local Similarity 80.6%; Pred. No. 1.7e-85;

Matches 208; Conservative 22; Mismatches 28; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGYRTGMSKTKNGITCQKWSSTSPHRPSPATHPSGLSEENYCRNPDN 60

Db 98 VYLSECKTGNGKNGYRTGMSKTKNGITCQKWSSTSPHRPSPATHPSGLSEENYCRNPDN 157

QY 61 DQGPWCYTTDEPKRYDYCDILECEBECMHCSENGYDGIKSTMSGLCQAWDSQSPHAH 120

Db 158 DQGPWCYTTDEPKRYDYCDILECEBECMHCSENGYDGIKSTMSGLCQAWDSQSPHAH 217

QY 121 GYIPSKFPNKLKKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTTPPPSSGPTTQCLK 180

Db 218 GYIPSKFPNKLKKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTTPPPSSGPTTQCLK 277

QY 181 GTGENYRGNAVTVSGHTCQHWSAQTPHTHTPFPCKNLDENYCRNPDGKRAPWCHT 240

Db 278 GRGENYRGNAVTVSGHTCQHWSAQTPHTHTPFPCKNLDENYCRNPDGKRAPWCHT 337

QY 241 TNSQVRWEYCKIPSCDSS 258

Db 338 TDSQVRWEYCKIPSCSS 355

RESULT 6

I46260

Plasmin (EC 3.4.21.7) precursor - western European hedgehog

C:Species: Echinacea europaea (western European hedgehog)

C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004

C:Accession: I46260

R:Lawn, R.M.; Boommark, N.W.; Schwartz, K.; Lindahl, G.E.; Wade, D.P.; Byrne, C.D.; Fong, J. Biol. Chem. 270, 24004-24009, 1995

A:Title: The recurring evolution of Lp(a): Insights from cloning of hedgehog apolipoprotein

A:Reference number: I46259; MUID:96025778; PMID:7592597

A:Accession: I46260

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-810 <LAW>

A:Cross-references: UNIPROT:Q29485; UNIPARC:UPI0000131C0D; EMBL:U33171; NID:g1046360; PI

C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology

C:Keywords: hydrolase; serine proteinase

F:1-96/Domain: plasminogen-related protein precursor homology <PLPH>

F:103-181/Domain: kringle homology <KR1>

F:185-262/Domain: kringle homology <KR2>

F:275-352/Domain: kringle homology <KR3>

F:379-456/Domain: kringle homology <KR4>

F:482-561/Domain: kringle homology <KR5>

F:582-803/Domain: trypsin homology <TRY>

Query Match 80.3%; Score 1237; DB 2; Length 810;

Best Local Similarity 77.9%; Pred. No. 8.4e-83;

Matches 201; Conservative 26; Mismatches 31; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGYRTGMSKTKNGITCQKWSSTSPHRPSPATHPSGLSEENYCRNPDN 60

Db 98 MYLSECKVGNGYRTGMSKTKNGITCQKWSSTSPHRPSPATHPSGLSEENYCRNPDN 157

QY 61 DQGPWCYTTDEPKRYDYCDILECEBECMHCSENGYDGIKSTMSGLCQAWDSQSPHAH 120

Db 158 DQGPWCYTTDEPKRYDYCDILECEBECMHCSENGYDGIKSTMSGLCQAWDSQSPHAH 217

QY 121 GYIPSKFPNKLKKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTTPPPSSGPTTQCLK 180

Db 218 GYIPSKFPNKLKKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTTPPPSSGPTTQCLK 277

QY 181 GTGENYRGNAVTVSGHTCQHWSAQTPHTHTPFPCKNLDENYCRNPDGKRAPWCHT 240

Db 278 GNGHYQGNVAVTVSGHTCQHWSAQTPHTHTPFPCKNLDENYCRNPDGKRAPWCHT 337

QY 241 TNSQVRWEYCKIPSCDSS 258

Db 338 TNSQVRWEYCKIPDCVSS 355

RESULT 7

T18518

apolipoprotein(a) - western European hedgehog (fragment)

C:Species: Echinacea europaea (western European hedgehog)

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T18518

R:Lawn, R.M.; Boommark, N.W.; Schwartz, K.; Lindahl, G.E.; Wade, D.P.; Byrne, C.D.; Fong, J. Biol. Chem. 270, 24004-24009, 1995

A:Title: The recurring evolution of Lp(a): Insights from cloning of hedgehog apolipoprotein

A:Reference number: I46259; MUID:96025778; PMID:7592597

A:Accession: T18518

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-2869 <LAW>

A:Cross-references: UNIPROT:Q28398; UNIPARC:UPI000008785C; EMBL:U33170; NID:g1046358; PI

A:Experimental source: liver

C:Comment: The lipoprotein Lp(a), a major inherited risk factor for atherosclerosis, consists of

apolipoprotein(a).

Query Match 57.2%; Score 881; DB 2; Length 2869;

Best Local Similarity 55.0%; Pred. No. 2.7e-56;

Matches 149; Conservative 36; Mismatches 70; Indels 16; Gaps 3;

QY 3 LSECKTGNGKNGYRTGMSKTKNGITCQKWSSTSPHRPSPATHPSGLSEENYCRNPDNDP 62

Db 2495 VDQCLEGTGNGKNGYRTGMSKTKNGITCQKWSSTSPHRPSPATHPSGLSEENYCRNPDNDP 2553

QY 63 QGPWCYTTDEPKRYDYCDILECEBECMHCSENGYDGIKSTMSGLCQAWDSQSPHAH 110

Db 2554 VAPVCYTTNSAVRWEYCKIPSCDSS 2613

QY 111 AWDSQSPHAHGYIPSKFPNKLKKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTTPPP 170

Db 2614 GWRKQTPHREYTPENYPSKNGYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTTPPP 2673

QY 171 SSGPTY---CQLKGTGNGKNGYRTGMSKTKNGITCQKWSSTSPHRPSPATHPSGLSEENYCRNPDNDP 227

Db 2674 PTEPMIIPDQCLEGTGNGKNGYRTGMSKTKNGITCQKWSSTSPHRPSPATHPSGLSEENYCRNPDNDP 2733

QY 228 RNPDKGRAPWCHTNSQVRWEYCKIPSCDSS 258

Db 2734 RNPDKGRAPWCHTNSQVRWEYCKIPSCSS 2764

RESULT 8
 JH0579
 hepatocyte growth factor precursor [validated] - human
 N:Alternate names: heparin-binding A; scatter factor
 C:Species: Homo sapiens (man)
 C>Date: 17-Aug-1992 #sequence revision 17-Aug-1992 #text change 09-Jul-2004
 C:Accession: JH0579; J03333; A41140; B36677; A33512; A39006; PH0114; A37796; S06799; T.; Hagiya, M.; Shimonishi, M.; Nakamura, T.; Shimizu, S.
 R:Seki, T.; Hagiya, M.; Shimonishi, M.; Nakamura, T.; Shimizu, S.
 Gene 102, 213-219, 1991
 A:Title: Organization of the human hepatocyte growth factor-encoding gene.
 A:Reference number: JH0579; MUID:91340155; PMID:1831432
 A:Accession: JH0579
 A:Molecule type: DNA
 A:Residues: 1-728 <SEK>
 A:Cross-references: UNIPROT:P14210; UNIPARC:UPI000000D92B; DBJ:D90318
 A>Note: the authors translated the codon GAA for residue 662 as Gly
 R:Seki, T.; Hagiya, M.; Shimonishi, M.; Nakamura, T.; Shimizu, S.
 submitted to JIPID, March 1991
 A:Description: Organization of the human hepatocyte growth factor-encoding gene.
 A:Reference number: JH0579
 A:Accession: JH0579
 A:Molecule type: DNA
 A:Residues: 1-481, 'RT', 484-728 <SE2>
 A:Cross-references: UNIPARC:UPI0000172B97
 R:Weidner, K.M.; Arakaki, N.; Hartmann, G.; Vandekerckhove, J.; Weingart, S.; Rieder, H.
 Proc. Natl. Acad. Sci. U.S.A. 88, 7001-7005, 1991
 A:Title: Evidence for the identity of human scatter factor and human hepatocyte growth factor.
 A:Reference number: A41140; MUID:91334393; PMID:1831266
 A:Accession: A41140
 A:Molecule type: mRNA
 A:Residues: 1-728 <WEI>
 A:Cross-references: UNIPARC:UPI000000D92B; GB:M73239; NID:G337935; PIDN:AAAS4239.1; PID:
 R:Seki, T.; Ihara, I.; Sugimura, A.; Shimonishi, M.; Nishizawa, T.; Asami, O.; Hagiya, M.
 Biochem. Biophys. Res. Commun. 172, 321-327, 1990
 A:Title: Isolation and expression of cDNA for different forms of hepatocyte growth factor.
 A:Reference number: A36677; MUID:91025062; PMID:2145936
 A:Accession: B36677
 A:Molecule type: mRNA
 A:Residues: 1-728 <SE3>
 A:Cross-references: UNIPARC:UPI000000D92B; GB:M60718; NID:G184031; PIDN:AAAS2648.1; PID:
 A:Accession: A36677
 A:Molecule type: mRNA
 A:Residues: 1-161, 167-728 <SE4>
 A:Cross-references: UNIPARC:UPI0000146316; EMBL:X16323
 A:Experimental source: leukocyte
 R:Miyazawa, K.; Tsubouchi, H.; Naka, D.; Takahashi, K.; Okigaki, M.; Arakaki, N.; Nakaya
 Biochem. Biophys. Res. Commun. 163, 967-973, 1989
 A:Title: Molecular cloning and sequence analysis of cDNA for human hepatocyte growth factor.
 A:Reference number: A33512; MUID:89392017; PMID:2528952
 A:Accession: A33512
 A:Molecule type: mRNA
 A:Status: not compared with conceptual translation
 A:Residues: 1-728 <MIY>
 A:Cross-references: UNIPARC:UPI000000D92B; GB:M29145; NID:G184041; PIDN:AAAS2650.1; PID:
 R:Rubin, J.S.; Chan, A.M.L.; Botcaro, D.P.; Burgess, W.H.; Taylor, W.G.; Cech, A.C.; Hir
 Proc. Natl. Acad. Sci. U.S.A. 88, 415-419, 1991
 A:Title: A broad-spectrum human lung fibroblast-derived mitogen is a variant of hepatocyte growth factor.
 A:Reference number: A39006; MUID:91110540; PMID:1824873
 A:Accession: A39006
 A:Molecule type: mRNA
 A:Residues: 1-161, 167-728 <RUB>
 A:Cross-references: UNIPARC:UPI0000146316; GB:M55379
 A:Experimental source: embryonic lung
 R:Yoshiyama, Y.; Arakaki, N.; Naka, D.; Takahashi, K.; Hirono, S.; Kondo, J.; Nakayama, M.
 Biochem. Biophys. Res. Commun. 175, 660-667, 1991
 A:Title: Identification of the N-terminal residue of the heavy chain of both native and recombinant human hepatocyte growth factor.
 A:Reference number: PH0114; MUID:91207365; PMID:1826837
 A:Accession: PH0114
 A:Molecule type: protein
 A:Residues: 32-43; 53-58 <YOS>
 A:Cross-references: UNIPARC:UPI0000172B98; UNIPARC:UPI0000172B99

A:Experimental source: plasma
 R:Weidner, K.M.; Behrens, J.; Vandekerckhove, J.; Birchmeier, W.
 J. Cell Biol. 111, 2097-2108, 1990
 A:Title: Scatter factor: molecular characteristics and effect on the invasiveness of epithelial cells.
 A:Reference number: A37796; MUID:91035621; PMID:2146276
 A:Accession: A37796
 A:Molecule type: protein
 A:Residues: 86-91; 329-344; 356-363, 'XX', 366-370; 425-434; 442-447, 'X', 449-450; 543-546, 'X', 54
 A:Cross-references: UNIPARC:UPI0000172B9A; UNIPARC:UPI0000172B9B; UNIPARC:UPI0000172B9C;
 R:Nakamura, T.; Nishizawa, T.; Hagiya, M.; Seki, T.; Shimonishi, M.; Sugimura, A.; Tashii
 Nature 342, 440-443, 1989
 A:Title: Molecular cloning and expression of human hepatocyte growth factor.
 A:Reference number: S06794; MUID:90066676; PMID:2531289
 A:Accession: S06794
 A:Molecule type: mRNA
 A:Residues: 1-31, 'HK', 34-77, 'N', 79-292, 'V', 294-299, 'W', 301-316, 'A', 318-335, 'K', 337-386, 'N'
 A:Cross-references: UNIPARC:UPI000015624E; EMBL:X16323; NID:G32081; PIDN:CAAS4387.1; PID:
 A:Experimental source: liver
 A>Note: the authors translated the codon CAG for residue 727 as Glu
 R:Hartmann, G.; Naldini, L.; Weidner, K.M.; Sachs, M.; Vigna, E.; Comoglio, P.M.; Birchmeier, H.
 Proc. Natl. Acad. Sci. U.S.A. 89, 11574-11578, 1992
 A:Title: A functional domain in the heavy chain of scatter factor/hepatocyte growth factor.
 A:Reference number: I59214; MUID:93087571; PMID:1280830
 A:Accession: I59214
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-288, 'ET', <HAR>
 A:Cross-references: UNIPARC:UPI0000073BF9; GB:L02931; NID:G184033; PIDN:AAAS2649.1; PID:
 R:Miyazawa, K.; Kitamura, A.; Naka, D.; Kitamura, N.
 Eur. J. Biochem. 197, 15-22, 1991
 A:Title: An alternatively processed mRNA generated from human hepatocyte growth factor gene.
 A:Reference number: S15443; MUID:91200041; PMID:1826653
 A:Accession: S15443
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-288, 'ET', <MIY2>
 A:Cross-references: UNIPARC:UPI0000073BF9; EMBL:X57574; NID:G32083; PIDN:CAAS40802.1; PID:
 R:Shima, N.; Nagao, M.; Ogaki, F.; Tsuda, E.; Murakami, A.; Higashio, K.
 Biochem. Biophys. Res. Commun. 180, 1151-1158, 1991
 A:Title: Tumor cytotoxic factor/hepatocyte growth factor from human fibroblasts: cloning and expression of cDNA.
 A:Reference number: I52253; MUID:92062058; PMID:1835383
 A:Accession: I52253
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 161-166 <SHI>
 A:Cross-references: UNIPARC:UPI00000353AB; GB:S62561; NID:G237996; PIDN:AAB20169.1; PID:
 C:Genetics:
 A:Gene: GDB:HGF
 A:Cross-references: GDB:127524; OMIM:142409
 A:Map position: 7q21.1-7q21.1
 A:Introns: 30/1; 85/2; 123/1; 161/2; 209/1; 249/2; 289/1; 347/2; 390/1; 424/2; 469/1; 481/2
 C:Complex: disulfide-bonded heterodimer of chains derived from the same precursor
 C:Function:
 A:Description: stimulates mitosis of hepatocytes and other cells
 A>Note: does not have proteinase activity
 C:Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringlike homologs
 C:Keywords: alternative splicing; glycoprotein; growth factor; heterodimer; kringlike; pyro
 F:1-31/Domain: signal sequence #status predicted <SIG>
 F:32-494, 495-728/Product: hepatocyte growth factor #status experimental <MAT>
 F:32-494/Domain: alpha chain #status experimental <ACH>
 F:128-206/Domain: kringlike homology <KR1>
 F:211-288/Domain: kringlike homology <KR2>
 F:305-383/Domain: kringlike homology <KR3>
 F:391-469/Domain: kringlike homology <KR4>
 F:495-728/Domain: beta chain #status experimental <BCH>
 F:495-716/Domain: trypsin homology <TRY>
 F:32/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experiment
 F:294, 402, 566, 653/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:487-604/Disulfide bonds: #status predicted
 Query Match 51.8%; Score 797; DB 1; Length 728;
 Best Local Similarity 51.0%; Pred. No. 9.4e-51;

[illegible]

F:489-716/Domain: macrophage-stimulating protein 1 beta chain #status predicted <BCH>
F:489-709/Domain: trypsin homology <TRI>
F:72,305,620/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 49.0%; Score 766.5; DB 1; Length 716;
Best Local Similarity 48.5%; Pred. No. 1.5e-48;
Matches 132; Conservative 36; Mismatches 89; Indels 15; Gaps 5;

QY 2 YLSECKTGNKGNVGTMSKTNGITCKQWSSSPHPRSPRSPATHPSEGLEENYCRNPND 61
DB 106 YVRTCIMDNGSVRGTVARTAGLPCQWSSRRFPNDHKYTF--PKNGLEENFCRNPDDG 163
QY 62 PQGPWCYTTDPKRYDYCDILECEE-EMHCSGENYDGIKSKTMSGLEQWDSQSPH 120
DB 164 PRGPWCYTTNRSVRPQSGIKCREAVCVWNGEDYRGEVDVTSRGECQWDLQPHSH 223
QY 121 GYIPSKFPNNLKKNYCRNPDRRLPWCFTTDPNKRWELCDIPRC--TTPPSSGTYQ- 177
DB 224 PFHPEKFPDKALKNDYCRNPDSASERPCWCTTDPNVEREFCDLPSCGPNLPPTTKGSKSQ 283
QY 178 -----CLKGTGENYRGNVAVTSGHTCOHWSAQTPHTHTERTPENFCNLDENYCRN 229
DB 284 RNKVRASNCFRGKGYRGTWNTTSAGVPCQWDAQNPQHFRVPEKYACKDLRENFERN 343
QY 230 PDGKRAPWCHTNSQVRWEYC-KIPSCDSSPV 260
DB 344 PDGSEAPWCFTRPGLRVAFQIPRCTEEV 375

RESULT 13

I51285

hepatocyte growth factor/scatter factor - chicken (fragment)

C:Species: Gallus gallus (chicken)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: I51285
R:Streit, A.; Stein, C.D.; Thery, C.; Ireland, G.W.; Aparicio, S.; Sharpe, M.J.; Gherard
Development 121, 813-824, 1995
A:Title: A role for HGF/SP in neural induction and its expression in Hensen's node durin
A:Reference number: I51285; MUID:95237013; PMID:7720585
A:Accession: I51285
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-411 <STR>

A:Cross-references: UNIPROT:Q90978; UNIPARC:UPI0000175C78; GB:S77480; NID:9998675; PID:9
C:Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringie homol
F:124-197/Domain: kringie homology <KR3>
F:202-279/Domain: kringie homology <KR2>
F:296-374/Domain: kringie homology <KR3>

Query Match 49.0%; Score 754.5; DB 2; Length 411;

Best Local Similarity 50.2%; Pred. No. 6.7e-48;

Matches 132; Conservative 31; Mismatches 89; Indels 11; Gaps 4;

QY 2 YLSECKTGNKGNVGTMSKTNGITCKQWSSSPHPRSPRSPATHPSEGLEENYCRNPND 61
DB 120 YVRCNLIIGKAEYKGTISITKSGIQQWNSMIPHE-----HSYRKDLRENYCRNPGE 174

QY 62 PQGPWCYTTDPKRYDYCDILECEE-EMHCSGENYDGIKSKTMSGLEQWDSQSPH 120
DB 175 EGGPWCFTTSPQWRHEVCDIPLCSEVECTMGESYRGPMDHTESKEQWDLQPHKH 234

QY 121 GYIPSKFPNNLKKNYCRNPDRRLPWCFTTDPNKRWELCDIPRC-----GPTY 176
DB 235 KFRPERYPDKGDDNYCRNPDKGLRPWCYTLDPNTEWFECAIKTCDVGLNSTEVAETT 294

QY 177 QCLKGTGENYRGNVAVTSGHTCOHWSAQTPHTHTERTPENFCNLDENYCRNPDKRAP 236
DB 295 TCIQGGEGYRGTWNTTSAGVPCQWDSQFPQHNTIPNFKKDLRENYCRNPDSGESP 354

QY 237 WCHTNSQVRWEYC-KIPSCDSS 258

DB 355 WCFTTDPNIRIGCSQIPKCDVS 377

RESULT 14

A40332

macrophage-stimulating protein 1 precursor - mouse

N:Alternate names: hepatocyte growth factor-like protein
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
C:Accession: A40332; B40332
R:Deegen, S.J.F.; Stuart, L.A.; Han, S.; Jamison, C.S.
Biochemistry 30, 9781-9791, 1991
A:Title: Characterization of the mouse cDNA and gene coding for a hepatocyte growth factor
A:Reference number: A40332; MUID:92002017; PMID:1832957

A:Accession: A40332

A:Molecule type: DNA

A:Residues: 1-716 <DEG>

A:Cross-references: UNIPROT:P26928; UNIPARC:UPI000000402E; GB:M74180; NID:g193831; PID:N
A:Accession: B40332

A:Molecule type: mRNA

A:Residues: 1-18, 'p', 20-716 <DEG2>

A:Cross-references: UNIPARC:UPI0000027E40; GB:M74181; NID:g193833; PIDN:AAAS0167.1; PID:5
C:Genetics:

A:Introns: 18/1; 67/2; 105/1; 143/2; 189/1; 229/2; 269/1; 334/2; 378/1; 412/2; 458/1; 470
C:Complex: disulfide-bonded heterodimer of chains derived from the same precursor
C:Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringie homolo
C:Keywords: duplication; glycoprotein; growth factor; kringie
F:1-31/Domain: signal sequence #status predicted <SIG>
F:19-488,489-716/Product: macrophage-stimulating protein 1 #status experimental <MAT>
F:19-483/Domain: alpha chain #status experimental <ACH>
F:110-186/Domain: kringie homology <KR1>
F:191-268/Domain: kringie homology <KR2>
F:292-370/Domain: kringie homology <KR3>
F:379-457/Domain: kringie homology <KR4>
F:484-711/Domain: beta chain #status experimental <BCH>
F:489-709/Domain: trypsin homology <TRY>
F:72,173,305,620/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 48.9%; Score 753.5; DB 1; Length 716;

Best Local Similarity 48.3%; Pred. No. 1.4e-47;

Matches 129; Conservative 37; Mismatches 86; Indels 15; Gaps 5;

QY 2 YLSECKTGNKGNVGTMSKTNGITCKQWSSSPHPRSPRSPATHPSEGLEENYCRNPND 61
DB 106 YVRTCIMDNGSVRGTVARTAGLPCQWSSRRFPNDHKYTF--PKNGLEENFCRNPDDG 163

QY 62 PQGPWCYTTDPKRYDYCDILECEE-EMHCSGENYDGIKSKTMSGLEQWDSQSPH 120
DB 164 PRGPWCYTTNRSVRPQSGIKCREAVCVLNGEDYRGEVDVTSRGECQWDLQPHSH 223

QY 121 GYIPSKFPNNLKKNYCRNPDRRLPWCFTTDPNKRWELCDIPRC--TTPPP----- 170
DB 224 PFQPEKFLDKLDKONYCRNPDSGSRPCWCTTDPNVEREFCDLPSCGPNLPPTTKGSKSQ 283

QY 171 -SSGPTYQCLKGTGENYRGNVAVTSGHTCOHWSAQTPHTHTERTPENFCNLDENYCRN 229
DB 284 RNKGAALNCFRGKGYRGTWNTTSAGVPCQWDAQSPQHFRVPEKYACKDLRENFERN 343

QY 230 PDGKRAPWCHTNSQVRWEYC-KIPSC 255

DB 344 PDGSEAPWCFTRPGLRVAFQIPRC 370

RESULT 15

S00657

apoptoteine(a) (BC 3.4.21.-) precursor [validated] - human

N:Alternate names: apolipoprotein(a); lipoprotein(a) chain apo(a)

C:Species: Homo sapiens (man)
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C:Accession: S00657; A28017; A47277; I60906; A47233; I52415; I65286
R:McLean, J.W.; Tomlinson, J.E.; Kuang, W.J.; Eaton, D.L.; Chen, E.Y.; Fless, G.M.; Scan
Nature 330, 132-137, 1987

A:Title: cDNA sequence of human apolipoprotein(a) is homologous to plasminogen.

A:Reference number: S00657; MUID:88039109; PMID:3670400

A:Accession: S00657

F	1396-1473/Domain:	kringle homology <KR13>	
F	1510-1587/Domain:	kringle homology <KR14>	
F	1624-1701/Domain:	kringle homology <KR15>	
F	1738-1815/Domain:	kringle homology <KR16>	
F	1852-1929/Domain:	kringle homology <KR17>	
F	1966-2043/Domain:	kringle homology <KR18>	
F	2080-2157/Domain:	kringle homology <KR19>	
F	2194-2271/Domain:	kringle homology <KR20>	
F	2308-2385/Domain:	kringle homology <KR21>	
F	2422-2499/Domain:	kringle homology <KR22>	
F	2536-2613/Domain:	kringle homology <KR23>	
F	2650-2727/Domain:	kringle homology <KR24>	
F	2764-2841/Domain:	kringle homology <KR25>	
F	2878-2955/Domain:	kringle homology <KR26>	
F	2992-3069/Domain:	kringle homology <KR27>	
F	3106-3183/Domain:	kringle homology <KR28>	
F	3220-3297/Domain:	kringle homology <KR29>	
F	3334-3411/Domain:	kringle homology <KR30>	
F	3448-3525/Domain:	kringle homology <KR31>	
F	3562-3639/Domain:	kringle homology <KR32>	
F	3676-3753/Domain:	kringle homology <KR33>	
F	3782-3859/Domain:	kringle homology <KR34>	
F	3896-3973/Domain:	kringle homology <KR35>	
F	4010-4087/Domain:	kringle homology <KR36>	
F	4124-4201/Domain:	kringle homology <KR37>	
F	4228-4307/Domain:	kringle homology <KR38>	
F	4328-4541/Domain:	trypsin homology <TRY>	
Query Match 48.6%; Score 749; DB 1; Length 4548;			
Best Local Similarity 41.2%; Pred. No. 1.8e-46;			
Matches 129; Conservative 45; Mismatches 81; Indels 58; Gaps 5;			
Qy	3	LSECKTGNGKNGYRGTMKTKNGITCKQWSTSPHRRPRFSPATHPSGLENYCRNPNDP	62
Db	3779	VQPCYHGDSQSRGSPSTTVGRTQCSWSMTPHWHQRTTEYPNGLITRNYCRNPDAEI	3838
Qy	63	QGPWCYTTPKEKYDCDILECE-----ECCM	89
Db	3839	R-PWCYTMDSVRWEYCNLTQCPVMGSLTTTPTVVPVSTELPSEAPTENSTGVQDCY	3897
Qy	90	HCSENGYDGKISMTSGLEQWDSQPHAGYIPSKFPNKNLKNYCRNPDRRLRPWCF	149
Db	3898	RGDSQYRGTLSTITIGRTQCSWSMTPHWHRIPLYYPNAGLITRNYCRNPDAEIRPCY	3957
Qy	150	TTDPNKRWELCDIPRC-----TTP-----PPSGPTVQ-CLKGTGEN	185
Db	3958	TMDPSVRWEYCNLTTRCFVTSESSVLTPTVAPVPSTEAPSEQAPPEKSPVQDCYHGDGRS	4017
Qy	186	YRCNGVATVSGHTQCSWQAQTPHTHERTPENFPCKNLDENYCRNPDGKRAPWCHTINSQV	245
Db	4018	YRGISSTTVGRTQCSWSMIPHWHQRTPENYPNAGLITRNYCRNPDSGQPCWCTTDPVCV	4077
Qy	246	RWEYCKIPSCDSS	258
Db	4078	RWEYCNLTCCSET	4090

Search completed: August 29, 2006, 14:01:59
Job time : 40 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 29, 2006, 13:51:34 ; Search time 199 Seconds
(without alignments)
597.368 Million cell updates/sec

Title: US-09-502-176-2

Perfect score: 1540

Sequence: 1 VYLSEKTEGKNGYRTGMSK.....TNSQVRWEYCKIPCDSSPV 260

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*
9: Geneseqp2005s:*
10: Geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1540	100.0	260	3	AAB26486 Deglycosy
2	1540	100.0	260	4	AU01209 Human Ang
3	1537	99.8	869	7	Adk40316 C-termina
4	1537	99.8	869	7	Adk40314 N-termina
5	1535	99.7	260	6	AAG79748 Human pla
6	1535	99.7	268	2	AAY02109 A multifu
7	1535	99.7	285	2	AAY02102 A multifu
8	1535	99.7	339	2	AAR83961 Human pla
9	1535	99.7	339	2	AAW07581 N-Termina
10	1535	99.7	339	2	AAW94038 Human ang
11	1535	99.7	339	4	AAW50518 Human ang
12	1535	99.7	339	7	ADG47024 Human ang
13	1535	99.7	339	8	Adm11543 Human pla
14	1535	99.7	339	9	AED08938 Human ang
15	1535	99.7	339	9	AED64669 Human ang
16	1535	99.7	363	3	AAV70255 Human ang
17	1535	99.7	364	2	AAV02106 A multifu
18	1535	99.7	374	3	AAV79226 Angiogene
19	1535	99.7	375	3	AAV79225 Angiogene
20	1535	99.7	378	2	AAW07579 Human kri
21	1535	99.7	378	3	AAW07579 Human kri
22	1535	99.7	378	5	AAW16450 Human ang
23	1535	99.7	378	7	ADG47063 Human kri

24	1535	99.7	378	9	AED08977 Human kri
25	1535	99.7	380	2	AAV02105 A multifu
26	1535	99.7	381	2	AAV02101 A multifu
27	1535	99.7	391	6	ADA08454 Mammalian
28	1535	99.7	391	8	ADP67426 A61 anti-
29	1535	99.7	394	6	ADA08455 Mammalian
30	1535	99.7	394	8	ADP67427 A61 anti-
31	1535	99.7	452	3	AAV79224 Angiogene
32	1535	99.7	453	2	AAV02093 A multifu
33	1535	99.7	453	2	AAV02099 A multifu
34	1535	99.7	453	2	AAV02095 A multifu
35	1535	99.7	453	2	AAV02096 A multifu
36	1535	99.7	453	2	AAW95051 Amino aci
37	1535	99.7	470	2	AAV02112 A multifu
38	1535	99.7	480	7	ABU64288 Human ang
39	1535	99.7	484	6	AAG79749 Human pla
40	1535	99.7	563	5	ABB75942 Endotheli
41	1535	99.7	566	2	AAV02100 A multifu
42	1535	99.7	571	5	ABB75944 Angiotens
43	1535	99.7	576	5	ABB75943 Angiotens
44	1535	99.7	579	8	ADG82532 Prolactin
45	1535	99.7	654	8	ABM83810 Human dia

ALIGNMENTS

RESULT 1
AAB26486
ID AAB26486 standard; protein; 260 AA.
AC AAB26486;
XX
DT 16-JAN-2001 (first entry)
XX
DS Deglycosylated kringle 1-5 region protein.
XX
KW Deglycosylated; kringle; angiogenesis; human.
XX
OS Homo sapiens.
XX
PN WO200047729-A1.
XX
PD 17-AUG-2000.
XX
PF 10-FEB-2000; 2000WO-US003482.
XX
PR 10-FEB-1999; 99US-0119562P.
PR 07-APR-1999; 99US-0128062P.
XX
PA (ENTR-) ENTREMED INC.
PA (CHIL-) CHILDRENS MEDICAL CENT.
XX
PI Pirie-Shepherd S, Folkman MJ, Liang H, Macdonald NJ, Sim KL;
XX
DR WPI; 2000-579032/54.
XX
N-ESDB; AAA94906.
XX
PT Novel composition comprising deglycosylated fragments of kringle 1-5 regions of plasminogen linked to the glycosylated form, useful for inhibiting angiogenesis.
XX
XX Claim 7; Fig 1; 42pp; English.
XX
CC The present sequence is deglycosylated kringle 1-5 region protein.
CC Deglycosylated kringle 1-5 region protein has increased antiangiogenic activity as compared to glycosylated kringle 1-5 region protein. The deglycosylated kringle 1-5 region protein was isolated from human plasminogen by affinity chromatography
XX
SQ Sequence 260 AA;
Query Match 100.0%; Score 1540; DB 3; Length 260;

02 CC Local Similarity 100.0%; Pred. No. 1.1e-90; Mismatches 0; Indels 0; Gaps 0;
03 TM Mismatches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VYLSECKTGNGKNGYRGMTSKNGITCQKWSSTSPHPRSPATHPSGEGLEENYCRNPDN 60
DB 1 VYLSECKTGNGKNGYRGMTSKNGITCQKWSSTSPHPRSPATHPSGEGLEENYCRNPDN 60
QY 61 DPGPWCYTTDPKRYDYCDILECEECMHCSENGYDGKISKMTSGLECAWDSQSPH 120
DB 61 DPGPWCYTTDPKRYDYCDILECEECMHCSENGYDGKISKMTSGLECAWDSQSPH 120
QY 121 GYIPSKFPNKLKNGYCRNPDRELRCWCTTDPNKRWELCDIPRCTTPPSSGPTYOCLX 180
DB 121 GYIPSKFPNKLKNGYCRNPDRELRCWCTTDPNKRWELCDIPRCTTPPSSGPTYOCLX 180
QY 181 GTGENTRGNAVTVSGHTCQHWSAQTPTHTERTPENPPCKNLDENYCRNPDGKRAPWCHT 240
DB 181 GTGENTRGNAVTVSGHTCQHWSAQTPTHTERTPENPPCKNLDENYCRNPDGKRAPWCHT 240
QY 241 TNSQVRWEYCKIPSCDSSPV 260
DB 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 2

ID AAU01209 standard; protein; 260 AA.
XX AAU01209;
XX
DT 26-SEP-2001 (first entry)
DE Human Angiostatin (hAsv3) protein.
XX Human; Angiostatin; recombinant production; cation exchange column;
KW fermentation; angiogenesis mediated disease; leukaemia; tumour;
KW rheumatoid arthritis; plaque neovascularisation.
XX Homo sapiens.
XX
FN WO200140260-A2.
XX
PD 07-JUN-2001.
XX
PP 04-DEC-2000; 2000WO-US032843.
XX
PR 03-DEC-1999; 99US-0168919P.
XX
XX (ENTR-) ENTREMED INC.
XX
XX Madsen J, Liang H, Sim KL, Zhou X, Chang-Murad A, Boerner RJ;
PI Bermejo LL, Mistry FR, Schrimsher JL, Shepard SR;
XX
DR WPI; 2001-408277/43.
DR N-PSDB; AAS04181.
XX
PT Purifying recombinant angiostatin, involves applying fermented broth
PT containing angiostatin to expanded bed cation exchange column, and
PT exchange column, hydroxyapatite column, hydrophobic column and a
PT membrane.
XX
XX Example 1; Page 22; 49pp; English.
XX
XX The present sequence representing Angiostatin protein is given in an
CC invention providing a method for recombinant production, recovery and
CC purification of Angiostatin protein. Purification of recombinant
CC Angiostatin comprises applying crude fermentation broth containing the
CC protein to an expanded bed cation exchange column, eluting it, and
CC applying the eluate to anion exchange column, repeating the process of
CC eluting and applying, to hydroxyapatite column, hydrophobic column and
CC membrane, in order, and collecting fluid passing through the membrane.
CC Angiostatin is useful for treating angiogenesis mediated diseases,
CC including solid tumours, leukaemia, tumour metastases, benign tumours,

CC rheumatoid arthritis, psoriasis, ocular angiogenic diseases, Osler-Webber
CC syndrome, myocardial angiogenesis, plaque neovascularisation,
CC telangiectasia, haemophilic joints, angiofibroma and wound granulation.
CC As a centrifugation technique is not employed in the process, damage to
CC the cells with concomitant release of undesirable biological materials
CC such as cytochromes, pigments, enzymes, chemicals and other undesirable
CC cellular constituents and debris, is prevented. Large scale recovery and
CC purification of proteins is greater than that obtained from prior art
CC methods. Active Angiostatin can be stored in buffers for extended periods
CC of time, in vials or other containers, either in solution which may be
CC liquid or frozen, or lyophilised
XX
XX Sequence 260 AA;
SQ
Query Match 100.0%; Score 1540; DB 4; Length 260;
Best Local Similarity 100.0%; Pred. No. 1.1e-90; Mismatches 0; Indels 0; Gaps 0;
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VYLSECKTGNGKNGYRGMTSKNGITCQKWSSTSPHPRSPATHPSGEGLEENYCRNPDN 60
DB 1 VYLSECKTGNGKNGYRGMTSKNGITCQKWSSTSPHPRSPATHPSGEGLEENYCRNPDN 60
QY 61 DPGPWCYTTDPKRYDYCDILECEECMHCSENGYDGKISKMTSGLECAWDSQSPH 120
DB 61 DPGPWCYTTDPKRYDYCDILECEECMHCSENGYDGKISKMTSGLECAWDSQSPH 120
QY 121 GYIPSKFPNKLKNGYCRNPDRELRCWCTTDPNKRWELCDIPRCTTPPSSGPTYOCLX 180
DB 121 GYIPSKFPNKLKNGYCRNPDRELRCWCTTDPNKRWELCDIPRCTTPPSSGPTYOCLX 180
QY 181 GTGENTRGNAVTVSGHTCQHWSAQTPTHTERTPENPPCKNLDENYCRNPDGKRAPWCHT 240
DB 181 GTGENTRGNAVTVSGHTCQHWSAQTPTHTERTPENPPCKNLDENYCRNPDGKRAPWCHT 240
QY 241 TNSQVRWEYCKIPSCDSSPV 260
DB 241 TNSQVRWEYCKIPSCDSSPV 260
RESULT 3
ADK40316
ID ADK40316 standard; protein; 869 AA.
XX
XX ADK40316;
XX
XX
DT 06-MAY-2004 (first entry)
XX
XX C-terminal albumin-angiostatin fusion protein.
XX
XX Cytostatic; vaccine; albumin fusion protein;
KW angiogenesis inhibiting peptide; angiogenesis-dependent tumor; cancer;
KW collagen.
XX
XX Homo sapiens.
OS Synthetic.
XX
PN WO2003066085-A1.
XX
XX 14-AUG-2003.
XX
XX 07-FEB-2003; 2003WO-IB000433.
XX
XX 07-FEB-2002; 2002US-0355547P.
XX
XX (AVET) AVENTIS BEHRING GMBH.
PA (DELZ) DELTA BIOTECHNOLOGY LTD.
XX
XX Mertins P, Celik I, Kisker O, Sleep D, Hay J, Hauser H;
XX
XX WPI; 2003-731479/69.
DR N-PSDB; ADK40315.
XX
XX New albumin fusion protein comprising an angiogenesis inhibiting peptide
PT

PT and an albumin having an albumin activity, or their fragments or
 PT variants, useful for treating angiogenesis-dependent tumor, e.g. cancer.
 XX
 PS Disclosure; Fig 8; 136pp; English.
 XX
 CC The invention relates to an albumin fusion protein comprising an
 CC angiogenesis inhibiting peptide and an albumin having an albumin
 CC activity, or their fragments or variants. The albumin fusion proteins,
 CC compositions, vaccines and methods are useful for treating angiogenesis-
 CC dependent tumor, e.g. cancer. This sequence represents an C-terminal
 CC albumin-angiostatin fusion protein.
 XX
 SQ Sequence 869 AA;

Query Match 99.8%; Score 1537; DB 7; Length 869;
 Best Local Similarity 99.8%; Pred. NO. 5.1e-90;
 Matches 259; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VYLSECKTGNGKNGYRTGKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN 60
 DB 610 VYLSECKTGNGKNGYRTGKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN 669
 QY 61 DPOGWCYTTDPEKRYDYCDILLECEBECMHCSGENTDGKISKTMGLCOAWDSQSPH 120
 DB 670 DPOGWCYTTDPEKRYDYCDILLECEBECMHCSGENTDGKISKTMGLCOAWDSQSPH 729
 QY 121 GIYPSKFPNKLKKNYCRNPDRELRCWCTTDPNKRWELCDIPRCTTTPPPSSGPTTQCLK 180
 DB 730 GIYPSKFPNKLKKNYCRNPDRELRCWCTTDPNKRWELCDIPRCTTTPPPSSGPTTQCLK 789
 QY 181 GTGENTRGNAVTVSGHTCOHWSAQTPTHTERTPENFPCKNLNDENYCRNPDGKRAPWCHT 240
 DB 790 GTGENTRGNAVTVSGHTCOHWSAQTPTHTERTPENFPCKNLNDENYCRNPDGKRAPWCHT 849
 QY 241 TNSQVWEYCKIPSCDSSPV 260
 DB 850 TNSQVWEYCKIPSCDSSPV 869

RESULT 4
 ADK40314
 ID ADK40314 standard; protein; 869 AA.
 XX
 AC ADK40314;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE N-terminal angiostatin-albumin fusion protein.
 XX
 KW cytostatic; vaccine; albumin fusion protein;
 KW angiogenesis inhibiting peptide; angiogenesis-dependent tumor; cancer;
 KW collagen.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO2003066085-A1.
 XX
 PD 14-AUG-2003.
 XX
 PF 07-FEB-2003; 2003WO-IB000433.
 XX
 PR 07-FEB-2002; 2002US-0355547P.
 XX
 PA (AVET) AVENTIS BEHRING GMBH.
 PA (DELZ) DELTA BIOTECHNOLOGY LTD.
 XX
 PI Martins P, Celik I, Kisker O, Sleep D, Hay J, Hauser H;
 XX
 DR 2003-731479/69.
 DR N-PSDB; ADK40313.
 XX
 PT New albumin fusion protein comprising an angiogenesis inhibiting peptide
 XX

PT and an albumin having an albumin activity, or their fragments or
 PT variants, useful for treating angiogenesis-dependent tumor, e.g. cancer.
 XX
 PS Disclosure; Fig 6; 136pp; English.
 XX
 CC The invention relates to an albumin fusion protein comprising an
 CC angiogenesis inhibiting peptide and an albumin having an albumin
 CC activity, or their fragments or variants. The albumin fusion proteins,
 CC compositions, vaccines and methods are useful for treating angiogenesis-
 CC dependent tumor, e.g. cancer. This sequence represents an N-terminal
 CC angiostatin-albumin fusion protein.
 XX
 SQ Sequence 869 AA;

Query Match 99.8%; Score 1537; DB 7; Length 869;
 Best Local Similarity 99.8%; Pred. NO. 5.1e-90;
 Matches 259; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VYLSECKTGNGKNGYRTGKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN 60
 DB 25 VYLSECKTGNGKNGYRTGKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN 84
 QY 61 DPOGWCYTTDPEKRYDYCDILLECEBECMHCSGENTDGKISKTMGLCOAWDSQSPH 120
 DB 85 DPOGWCYTTDPEKRYDYCDILLECEBECMHCSGENTDGKISKTMGLCOAWDSQSPH 144
 QY 121 GIYPSKFPNKLKKNYCRNPDRELRCWCTTDPNKRWELCDIPRCTTTPPPSSGPTTQCLK 180
 DB 145 GIYPSKFPNKLKKNYCRNPDRELRCWCTTDPNKRWELCDIPRCTTTPPPSSGPTTQCLK 204
 QY 181 GTGENTRGNAVTVSGHTCOHWSAQTPTHTERTPENFPCKNLNDENYCRNPDGKRAPWCHT 240
 DB 205 GTGENTRGNAVTVSGHTCOHWSAQTPTHTERTPENFPCKNLNDENYCRNPDGKRAPWCHT 264
 QY 241 TNSQVWEYCKIPSCDSSPV 260
 DB 265 TNSQVWEYCKIPSCDSSPV 284

RESULT 5
 AAG79748
 ID AAG79748 standard; protein; 260 AA.
 XX
 AC AAG79748;
 XX
 DT 18-MAR-2003 (first entry)
 XX
 DE Human plasminogen kringle domains 1-3, Kl-3.
 XX
 KW Human; plasminogen; angiostatin; neovascularisation; kringle domain;
 KW cell proliferation; viral vector; replication-defective; cancer; tumour.
 XX
 OS Homo sapiens.
 XX
 PN WO200288173-A2.
 XX
 PD 07-NOV-2002.
 XX
 PF 29-APR-2002; 2002WO-US013461.
 XX
 PR 30-APR-2001; 2001US-0287673P.
 PR 05-APR-2002; 2002US-0370634P.
 XX
 PA (CELL-) CELL GENESYS INC.
 XX
 PI Chang B, Wu WW, Macarthur J, Patel S, Jooss K, Mendez M;
 XX
 DR WPI; 2003-129131/12.
 DR N-PSDB; ABA00776.
 XX
 PT New recombinant viral vector expressing human angiostatin useful for
 PT inhibiting angiogenesis in a mammalian subject with cancer or tumor.
 XX

PS closure; Page 75-76; 83pp; English.

XX This sequence represents kringle domains 1-3 of human plasminogen. A 38
CC kD N-terminal fragment of plasminogen is referred to as angiotatin and
CC inhibits neovascularisation. Angiotatin contains 4 kringle domains of
CC the parent molecule. However, angiotatin containing all 4 kringle
CC domains (K1-4) was found to be no more potent as an inhibitor of cell
CC proliferation than an angiotatin only containing K1-3. Therefore,
CC kringle 4 does not possess inhibitory activity. A fragment of the
CC plasminogen coding sequence may be used in the recombinant viral vector
CC of the invention for obtaining angiotatin activity. The vector comprises
CC a promoter capable of expressing human angiotatin operably linked to a
CC structural gene encoding one or more domains of human angiotatin. The
CC vector, which may be a replication-defective viral vector, is useful for
CC inhibiting angiogenesis in a mammal, especially with cancer or a tumour
XX

SQ Sequence 260 AA;

Query Match 99.7%; Score 1535; DB 6; Length 260;
Best Local Similarity 99.6%; Pred. No. 2.2e-90;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGNYRTGMSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN 60

DB 1 VYLSECKTGNGNYRTGMSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN 60

QY 61 DPQGPWCYTTDEPKRYDYCDILECEECMHCSENGYDGKISKTMGLCQAWDSQSPHAH 120

DB 61 DPQGPWCYTTDEPKRYDYCDILECEECMHCSENGYDGKISKTMGLCQAWDSQSPHAH 120

QY 121 GYIPSKFPNNLKKNYCRNPDRRLPWCFTTDPNKRWELCDIPRCTTPPPSSGFTYQCLK 180

DB 121 GYIPSKFPNNLKKNYCRNPDRRLPWCFTTDPNKRWELCDIPRCTTPPPSSGFTYQCLK 180

QY 181 GTGENYRGNAVTVSGHTCOHWSAQTPHTHTERTPENFPCKNLNDENYCRNPDGKRAPWCHT 240

DB 181 GTGENYRGNAVTVSGHTCOHWSAQTPHTHTERTPENFPCKNLNDENYCRNPDGKRAPWCHT 240

QY 241 TNSQVRWEYCKIPSCDSSPV 260

DB 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 6

AAY02109

ID AAY02109 standard; protein; 268 AA.

XX

AC AAY02109;

XX

DT 16-JUL-1999 (first entry)

XX A multifunctional protein of the invention.

XX Angiotatin; endostatin; interferon; thrombospondin;

KW interferon-inducible protein; platelet factor 4; anti-angiogenic;

KW anti-tumor; multifunctional protein; angiogenic-mediated disease; cancer;

KW diabetic retinopathy; macular degeneration; arthritis;

KW tumor cell production.

XX

OS Synthetic.

OS Homo sapiens.

XX

XX WO9916889-A1.

XX

XX 08-APR-1999.

XX

XX 30-SEP-1998; 98WO-US020464.

XX

XX 01-OCT-1997; 97US-0060609P.

XX

XX (SEAR) SEARLE & CO G D.

XX

XX Bolanowski MA, Caparon MH, Casperson GF, Gregory SA, Klein BK;

XX

PI McKeam JP;

XX

DR WPI; 1999-255098/21.

XX

XX New multifunctional proteins useful for treating angiogenic-mediated

PT diseases.

XX

XX Claim 5; Page 104; 121pp; English.

XX

CC The specification describes multifunctional proteins which comprise

CC combinations of angiotatin, endostatin, interferon, thrombospondin,

CC interferon-inducible protein and platelet factor 4, and have anti-

CC angiogenic and/or anti-tumor activity. The multifunctional protein may

CC exhibit useful properties such as having similar or greater biological

CC activity when compared to a single factor or by having improved half-life

CC or decreased adverse side effects, or a combination of these properties.

CC The proteins can be used for treating an angiogenic-mediated disease,

CC e.g. cancer, diabetic retinopathy, macular degeneration, or arthritis.

CC They can also be used for inhibiting the production of tumor cells

CC (characteristic of lung, breast, ovarian, prostate, pancreatic, gastric,

CC colon, renal, bladder cancers; melanoma, hepatoma, sarcoma and lymphoma)

CC in a patient and for inhibiting tumor growth. The present sequence

CC represents a multifunctional protein of the invention

XX

SQ Sequence 268 AA;

Query Match 99.7%; Score 1535; DB 2; Length 268;

Best Local Similarity 99.6%; Pred. No. 2.3e-90;

Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGNYRTGMSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN 60

DB 3 VYLSECKTGNGNYRTGMSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN 62

QY 61 DPQGPWCYTTDEPKRYDYCDILECEECMHCSENGYDGKISKTMGLCQAWDSQSPHAH 120

DB 63 DPQGPWCYTTDEPKRYDYCDILECEECMHCSENGYDGKISKTMGLCQAWDSQSPHAH 122

QY 121 GYIPSKFPNNLKKNYCRNPDRRLPWCFTTDPNKRWELCDIPRCTTPPPSSGFTYQCLK 180

DB 123 GYIPSKFPNNLKKNYCRNPDRRLPWCFTTDPNKRWELCDIPRCTTPPPSSGFTYQCLK 182

QY 181 GTGENYRGNAVTVSGHTCOHWSAQTPHTHTERTPENFPCKNLNDENYCRNPDGKRAPWCHT 240

DB 183 GTGENYRGNAVTVSGHTCOHWSAQTPHTHTERTPENFPCKNLNDENYCRNPDGKRAPWCHT 242

QY 241 TNSQVRWEYCKIPSCDSSPV 260

DB 243 TNSQVRWEYCKIPSCDSSPV 262

RESULT 7

AAY02102

ID AAY02102 standard; protein; 285 AA.

XX

AC AAY02102;

XX

XX 16-JUL-1999 (first entry)

XX

XX A multifunctional protein of the invention.

XX

XX Angiotatin; endostatin; interferon; thrombospondin;

KW interferon-inducible protein; platelet factor 4; anti-angiogenic;

KW anti-tumor; multifunctional protein; angiogenic-mediated disease; cancer;

KW diabetic retinopathy; macular degeneration; arthritis;

KW tumor cell production.

XX

OS Synthetic.

OS Homo sapiens.

XX

XX WO9916889-A1.

XX

XX 08-APR-1999.

XX

XX PF 30-SEP-1998; 98WO-US020464.
 XX PR 01-OCT-1997; 97US-0060609P.
 XX PA (SEAR) SEARLE & CO G D.
 XX PI Bolanowski MA, Caparon MH, Casperson GP, Gregory SA, Klein BK;
 XX PI McKearn JP;
 XX DR WPI; 1999-255098/21.
 XX PT New multifunctional proteins useful for treating angiogenic-mediated
 XX PT diseases.
 XX PS Claim 5; Page 97-98; 121pp; English.
 XX CC The specification describes multifunctional proteins which comprise
 CC combinations of angiotensin, endostatin, interferon, thrombospondin,
 CC interferon-inducible protein and platelet factor 4, and have anti-
 CC angiogenic and/or anti-tumor activity. The multifunctional protein may
 CC exhibit useful properties such as having similar or greater biological
 CC activity when compared to a single factor or by having improved half-life
 CC or decreased adverse side effects, or a combination of these properties.
 CC The proteins can be used for treating an angiogenic-mediated disease,
 CC e.g. cancer, diabetic retinopathy, macular degeneration, or arthritis.
 CC They can also be used for inhibiting the production of tumor cells
 CC (characteristic of lung, breast, ovarian, prostate, pancreatic, gastric,
 CC colon, renal, bladder cancers; melanoma, hepatoma, sarcoma and lymphoma)
 CC in a patient and for inhibiting tumor growth. The present sequence
 CC represents a multifunctional protein of the invention
 XX SQ Sequence 285 AA;
 Query Match 99.7%; Score 1535; DB 2; Length 285;
 Best Local Similarity 99.6%; Pred. No. 2.4e-90;
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 VYLSECKTGNGNYRGTMTKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN 60
 DB 20 VYLSECKTGNGNYRGTMTKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN 79
 QY 61 DPQGPWCYTTDPKRYDYCDILECEECMHCSENYDGKISKTMSGLECQAWDSQSPH 120
 DB 80 DPQGPWCYTTDPKRYDYCDILECEECMHCSENYDGKISKTMSGLECQAWDSQSPH 139
 QY 121 GYIPSPFPNKLKKNYCRNPDRELRCWCTTDPNKEWELCDIPRCTTPPPSSGPTYQCLK 180
 DB 140 GYIPSPFPNKLKKNYCRNPDRELRCWCTTDPNKEWELCDIPRCTTPPPSSGPTYQCLK 199
 QY 181 GTGENYRGNAVTVSGHTCOHWSAQTPHTHTPTNPENPCNLDENYCRNPDGKRAPWCHT 240
 DB 200 GTGENYRGNAVTVSGHTCOHWSAQTPHTHTPTNPENPCNLDENYCRNPDGKRAPWCHT 259
 QY 241 TNSQVREYCKIPSCDSSPV 260
 DB 260 TNSQVREYCKIPSCDSSPV 279
 RESULT 8
 AAR83961
 ID AAR83961 standard; protein; 339 AA.
 XX AC AAR83961;
 XX DT 10-MAR-1996 (first entry)
 XX PT Human plasminogen peptide fragment.
 XX PT angiotensin; plasminogen; endothelial inhibitor; therapeutic;
 XX PT gene therapy.
 XX OS Homo sapiens.

XX PN WO9529242-A1.
 XX PD 02-NOV-1995.
 XX PF 26-APR-1995; 95WO-US005107.
 XX PR 26-APR-1994; 94US-00248629.
 XX PR 20-OCT-1994; 94US-00328785.
 XX PA (CHIL-) CHILDRENS MEDICAL CENT.
 XX PI Oreilly MS, Folkman MJ, Sim KL, Cao Y;
 XX DR WPI; 1995-382990/49.
 XX PT Endothelial inhibitor Angiostatin - useful to treat angiogenic mediated
 XX PT disease esp. angiogenesis and cancer.
 XX PS Claim 4; Page 81-82; 108pp; English.
 XX CC The sequence represents a plasminogen fragment which is compared with the
 CC corresponding plasminogen fragments of monkey (AAR83962), pig (AAR83963)
 CC and cattle (AAR83964) origin (in Fig.2), as well as the with the first
 CC 339 amino acids of mouse angiotensin (AAR83960) (i.e. aa's 98-436 of the
 CC complete 812 aa plasminogen molecule AAR83959). Human angiotensin is a
 CC plasminogen fragment starting at aa 97 or 99 of the complete plasminogen
 CC molecule. Angiotensin is an endothelial inhibitor, which reversibly
 CC inhibits proliferation of endothelial cells and thereby inhibits
 CC angiogenesis. It is useful in the treatment of a human or animal with
 CC angiogenic mediated disease e.g. arthritis, macular degeneration,
 CC diabetic retinopathy or cancer. Cells comprising angiotensin-coding
 CC sequences are useful for gene therapy of primary tumors
 XX SQ Sequence 339 AA;
 Query Match 99.7%; Score 1535; DB 2; Length 339;
 Best Local Similarity 99.6%; Pred. No. 2.8e-90;
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 VYLSECKTGNGNYRGTMTKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN 60
 DB 1 VYLSECKTGNGNYRGTMTKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN 60
 QY 61 DPQGPWCYTTDPKRYDYCDILECEECMHCSENYDGKISKTMSGLECQAWDSQSPH 120
 DB 61 DPQGPWCYTTDPKRYDYCDILECEECMHCSENYDGKISKTMSGLECQAWDSQSPH 120
 QY 121 GYIPSPFPNKLKKNYCRNPDRELRCWCTTDPNKEWELCDIPRCTTPPPSSGPTYQCLK 180
 DB 121 GYIPSPFPNKLKKNYCRNPDRELRCWCTTDPNKEWELCDIPRCTTPPPSSGPTYQCLK 180
 QY 181 GTGENYRGNAVTVSGHTCOHWSAQTPHTHTPTNPENPCNLDENYCRNPDGKRAPWCHT 240
 DB 181 GTGENYRGNAVTVSGHTCOHWSAQTPHTHTPTNPENPCNLDENYCRNPDGKRAPWCHT 240
 QY 241 TNSQVREYCKIPSCDSSPV 260
 DB 241 TNSQVREYCKIPSCDSSPV 260
 RESULT 9
 AAW07581
 ID AAW07581 standard; protein; 339 AA.
 XX AC AAW07581;
 XX DT 24-JUN-1997 (first entry)
 XX PT N-Terminal angiotensin fragment.
 XX PT angiotensin; plasminogen; kringles; angiogenesis; cancer; arthritis;
 XX PT macular degeneration; diabetic retinopathy.

Human sapiens.
WO9635774-A2.
14-NOV-1996.
26-APR-1996; 96WO-US005856.
26-APR-1995; 95US-00429743.
22-FEB-1996; 96US-00605598.
08-MAR-1996; 96US-00612788.
(CHIL-) CHILDRENS MEDICAL CENT.
Folkman MJ, O'reilly MS, Cao Y, Sim XL, Lin J;
WPI; 1996-518662/51.
Use of angiotensin fragments or aggregates - for inhibiting endothelial cell proliferation and treating angiogenesis-mediated diseases, e.g. cancer, arthritis or diabetic retinopathy.
Claim 59; Page 96-97; 203pp; English.
The invention relates to new methods and compositions for inhibiting endothelial cell proliferation, using as active component an angiotensin fragment, a combination of angiotensin fragments, or aggregate angiotensin. The fragment is preferably derived from murine, human, Rhesus, porcine or bovine plasminogen and is a kringle 1, kringle 2, kringle 3, kringle 2-3, kringle 1-3, kringle 1-2, kringle 1-4 or kringle 1-4BLS protein. The aggregate angiotensin has a Mol. Wt. of 45-65 kD and is derived from a plasminogen fragment beginning at approximately amino acid number 98 of murine, human, Rhesus, porcine or bovine plasminogen. The active component can be used for treating angiogenesis-mediated diseases such as cancer, arthritis, macular degeneration and diabetic retinopathy. It can also be used to develop antibodies for use in diagnosis, detection and therapy. The present sequence, which is the N-terminal fragment of human angiotensin, is a specific aggregate angiotensin which can be used in the invention
Sequence 339 AA;
Query Match 99.7%; Score 1535; DB 2; Length 339;
Best Local Similarity 99.6%; Pred. No. 2.8e-90;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 VYLSECKTGNKNGYRGTMTSKNGITCQKWSSTSPHRPSPATHPSGLEENYCRNPDN 60
DB 1 VYLSECKTGNKNGYRGTMTSKNGITCQKWSSTSPHRPSPATHPSGLEENYCRNPDN 60
QY 61 DPGPWCYTTDPKRYDYCDILECEBECMHCSGENTYDGKISKTMSGLECQAWDSQSPHAH 120
DB 61 DPGPWCYTTDPKRYDYCDILECEBECMHCSGENTYDGKISKTMSGLECQAWDSQSPHAH 120
QY 121 GYTPSPFNKLNKNTCRNPDRELRCPCFTTDPNKEWELCDIPRCTTTPSSGPTVOCLEK 180
DB 121 GYTPSPFNKLNKNTCRNPDRELRCPCFTTDPNKEWELCDIPRCTTTPSSGPTVOCLEK 180
QY 181 GTGENTRGVAVTVSGHTCQHWASQTPHTHTERTPENFPCKNLNDEYCRNPDGKRAPWCHT 240
DB 181 GTGENTRGVAVTVSGHTCQHWASQTPHTHTERTPENFPCKNLNDEYCRNPDGKRAPWCHT 240
QY 241 TNSQVRWEYCKIPSCDSSPV 260
DB 241 TNSQVRWEYCKIPSCDSSPV 260
RESULT 10
AAW94038
ID AAW94038 standard; protein; 339 AA.
AC AAW94038;
XX

06-APR-1999 (first entry)
Human angiotensin fragment.
Plasminogen; kringle; endothelial; angiogenesis; tumour; leukaemia; rheumatoid arthritis; psoriasis; ocular angiogenic disease; ulcer; gene therapy; birth control; Crohn's disease; angiotensin.
Homo sapiens.
Key Location/Qualifiers
FT Peptide 6..255 /note= "Kringle 1-3"
FT Peptide 6..165 /note= "Kringle 1-2"
FT Peptide 6..84 /note= "Kringle 1"
FT Peptide 88..255 /note= "Kringle 2-3"
FT Peptide 88..165 /note= "Kringle 2"
FT Peptide 178..255 /note= "Kringle 3"
XX WO9854217-A1.
XX 03-DEC-1998.
XX 29-MAY-1998; 98WO-US010979.
XX 30-MAY-1997; 97US-00866735.
XX (CHIL-) CHILDRENS MEDICAL CENT.
XX Folkman MJ, O'reilly MS;
XX WPI; 1999-059809/05.
XX Use of plasminogen fragments - having an amino acid sequence similar to the kringle 1-5 region, for inhibiting endothelial cell proliferation and angiogenesis.
Example 27; Fig 2A-C; 165pp; English.
The invention relates to inhibition of endothelial cell proliferation that comprises administering to an endothelial cell a plasminogen fragment having an amino acid sequence similar to the kringle 1-5 region of a plasminogen molecule. The plasminogen fragments can be derived from murine, human, Rhesus, porcine or bovine plasminogens. The plasminogen fragments can be used for modulating angiogenesis and treating angiogenic-mediated disease e.g. solid tumours; for treating excessive or abnormal stimulation of endothelial cells; as a birth control agent; and in the treatment of diseases that have angiogenesis as a pathological consequence (see AAW94036 for details on the various diseases the plasminogen fragments can be used to treat). The nucleotide sequences encoding the plasminogen fragments can also be used for gene therapy. The products can be used for the production of antibodies and in detection and diagnosis. Sequences AAW94037 to W4041 represent angiotensin fragments (protein derivatives of angiotensin or plasminogen, having an endothelial cell proliferation activity) of murine, human, Rhesus, porcine and bovine angiotensins respectively. The kringle regions that can be used in the invention are indicated in the features
Sequence 339 AA;
Query Match 99.7%; Score 1535; DB 2; Length 339;
Best Local Similarity 99.6%; Pred. No. 2.8e-90;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 VYLSECKTGNKNGYRGTMTSKNGITCQKWSSTSPHRPSPATHPSGLEENYCRNPDN 60
DB 1 VYLSECKTGNKNGYRGTMTSKNGITCQKWSSTSPHRPSPATHPSGLEENYCRNPDN 60

QY 61 DPGQWCYTTDPEKRYDYCDILECEBCHMGCSGENYDGKISKTMGLCQAWDSQSPHAH 120
 DB 61 DPGQWCYTTDPEKRYDYCDILECEBCHMGCSGENYDGKISKTMGLCQAWDSQSPHAH 120
 QY 121 GYIPSKFPNKNLKNYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTTPPPSSGGTYQCLK 180
 DB 121 GYIPSKFPNKNLKNYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTTPPPSSGGTYQCLK 180
 QY 181 GTGENYRGNAVTVSGHTCQHWSAQTPHTHRTPEPFCNLDENYCRNPDGKRAPWCHT 240
 DB 181 GTGENYRGNAVTVSGHTCQHWSAQTPHTHRTPEPFCNLDENYCRNPDGKRAPWCHT 240
 QY 241 TNSQVRWEYCKIPSCDSSPV 260
 DB 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 11

AAM50518
 ID AAM50518 standard; protein; 339 AA.

XX AAM50518;

AC 12-MAR-2002 (first entry)
 DT
 XX Human angiotatin.

XX Angiotatin; plasminogen; human; angiogenesis; endothelial cell;
 KW cell proliferation; inhibitor; tumour; antipsoriatic; cytostatic;
 KW vasotropic; antitumour; dermatological; antiinflammatory; antidiabetic;
 KW antirheumatic; antiarthritic; ophthalmological; vulnery; antiulcer;
 KW antibacterial; antiatherosclerotic; gynaecological; antipyretic;
 KW cardiant; contraceptive; therapy.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT Region 6..255
 FT /label= Kringle-1-3
 FT Region 6..165
 FT /label= Kringle-1-2
 FT Region 6..84
 FT /label= Kringle-1
 FT Region 88..255
 FT /label= Kringle-2-3
 FT Region 88..165
 FT /label= Kringle-2
 FT Region 178..255
 FT /label= Kringle-3

XX US2001029246-A1.

XX 11-OCT-2001.

XX 16-FEB-2001; 2001US-00788142.

XX 30-MAY-1997; 97US-00866735.

XX 24-APR-1998; 98US-00066028.

XX 11-MAY-1999; 99US-00309821.

XX 22-JUN-1999; 99US-00338387.

XX (OREI//) O'REILLY M S.

XX (FOLK//) FOLKMAN M J.

XX (CAOY//) CAO Y.

XX O'reilly MS, Folkman MJ, Cao Y;

XX 2001-647990/74.

XX Angiotatin endothelial cell proliferation, useful for treating angiogenic
 PT mediated diseases such as cancer, arthritis, comprises administering
 PT plasminogen fragment corresponding to kringle structures of plasminogen

PT molecule.

XX Example 27; Fig 2A-C; 70pp; English.

XX The present sequence is that of human angiotatin. A claimed method of
 CC inhibiting endothelial cell proliferation involves administering a
 CC plasminogen fragment (PF) having an amino acid sequence similar to the
 CC kringle 1-5 region of a plasminogen molecule. This includes a protein,
 CC termed angiotatin, defined by its ability to overcome the angiogenic
 CC activity of endogenous growth factors and by its amino acid sequence
 CC homology and structural similarity to an internal portion of plasminogen,
 CC beginning at approximately amino acid 98. The PF is preferably derived
 CC from mouse, human, Rhesus monkey, pig or cattle (see AAM50516-21). It is
 CC used in methods and compositions for the treatment of an angiogenic-
 CC mediated disease, including haemangioma, solid tumours, blood-borne
 CC tumours, leukaemia, metastasis, telangiectasia, psoriasis,
 CC atherosclerosis, scleroderma, pyogenic granuloma, myocardial
 CC angiogenesis, Crohn's disease, plaque neovascularisation, coronary
 CC collaterals, cerebral collaterals, arteriovenous malformations, ischaemic
 CC limb angiogenesis, corneal diseases, rubeosis, neovascular glaucoma,
 CC diabetic retinopathy, corneal graft rejection, retrolental fibroplasia,
 CC haemophilic joints, rheumatoid arthritis, diabetic neovascularisation,
 CC Osler-Webber syndrome, macular degeneration, wound healing, peptic ulcer,
 CC Helicobacter pylori related diseases, fractures, keloids, vasculogenesis,
 CC haematopoiesis, ovulation, menstruation, placental and cat scratch
 CC fever. Angiotatin is also useful as a birth control agent by preventing
 CC vascularisation required for embryo implantation. The compositions are
 CC particularly useful for treating or repressing the growth of tumours.
 CC Administration of angiotatin to a human or animal with prevascularised
 CC metastasized tumours will prevent the growth or expansion of those
 CC tumours. Gene therapy methods are also included in the invention

XX Sequence 339 AA;

QY Query Match 99.7%; Score 1535; DB 4; Length 339;

DB Best Local Similarity 99.6%; Pred. No. 2.8e-90;

DB Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGRTGWTGKTKNGITCQKWSSTSPHRPRFSPATHPSGLENYCRNPDN 60

DB 1 VYLSECKTGNGKNGRTGWTGKTKNGITCQKWSSTSPHRPRFSPATHPSGLENYCRNPDN 60

QY 61 DPGQWCYTTDPEKRYDYCDILECEBCHMGCSGENYDGKISKTMGLCQAWDSQSPHAH 120

DB 61 DPGQWCYTTDPEKRYDYCDILECEBCHMGCSGENYDGKISKTMGLCQAWDSQSPHAH 120

QY 121 GYIPSKFPNKNLKNYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTTPPPSSGGTYQCLK 180

DB 121 GYIPSKFPNKNLKNYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTTPPPSSGGTYQCLK 180

QY 181 GTGENYRGNAVTVSGHTCQHWSAQTPHTHRTPEPFCNLDENYCRNPDGKRAPWCHT 240

DB 181 GTGENYRGNAVTVSGHTCQHWSAQTPHTHRTPEPFCNLDENYCRNPDGKRAPWCHT 240

QY 241 TNSQVRWEYCKIPSCDSSPV 260

DB 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 12

ADG47024

ID ADG47024 standard; protein; 339 AA.

XX ADG47024;

XX 11-MAR-2004 (first entry)

XX Human angiotatin protein.

XX Angiotatin; cell proliferation; angiogenic-mediated disease; cancer;
 KW arthritis; macular degeneration; diabetic retinopathy; psoriasis;
 KW scleroderma; Crohn's disease; wounds; peptic ulcer; fracture;
 KW gene therapy; plasminogen; cytostatic; ophthalmological; dermatological;

inflammatory; vulnery; human.

Hom sapiens.

US2003064926-A1.

03-APR-2003.

22-APR-2002: 2002US-00127066.

26-APR-1994:

20-AFK-1994;
20-OCT-1994;

26-APR-1995;

08-MAR-1996;

30-MAY-1997;

24-APR-1998;

11-MAY-1999;
17-MAY-1999;

17-JUN-1999;
22-JUN-1999;

22-JUN-1999;
16-FEB-2001;

1007-333-01

(FOLK/) FOLKMAN M J.

(OREI/) O'REILLY M S.

(CAOY/) CAO Y.

(SIMK/) SIM K L.

Folkman MJ, O'reilly MS, Cao Y, Sim KL;

WPI; 2003-540796/51.

Inhibiting endothelial cell proliferation, useful for treating cancer, arthritis or diabetic retinopathy, comprises administering to an endothelial cell a proliferation-inhibiting amount of an angiostatin fragment.

Example 27: SEO ID NO 3: 96pp: English.

The present invention relates to endothelial inhibitors called angiotatin which reversibly inhibit proliferation of endothelial cells. The invention is useful for diagnosing and treating angiogenic-mediated diseases such as cancer, arthritis, macular degeneration, diabetic retinopathy, psoriasis, scleroderma, Crohn's disease, wounds, peptic ulcer and fractures. The invention is also useful in gene therapy. The present sequence is the human angiotatin protein.

Sequence 339 AA:

99.7%: Score 1535: DB 7: Length 339:

Very Match
Best Local Similarity

Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 VYLSECKTGNGKQYRGTMSTKNGITCOKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN 60

1

THE HISTORY OF THE UNITED STATES

61 DPQGPWCYTTDPEKRYDYCDILECEEECMHCSENYDGKISKTMGLECQAWDSQSPHAH 120

61 DPOGPWCYTTPPEKRYDYCDILCEEEECMHCSGENYDGKISKTMGLECQAWDSQSPHAH 120

01 DE WENN U. VON

IZI G I F S A F P N N L R A N V I C K R V E D R E N F W C F I I D E N K X W E T C O I F A C U I T F F C O O L I A Y C U A I

121 GYIPSKFPNKLKNYCRNPDELRPWCFTTDPNKRWELCDIPRCTTTPPSSGPTYQCLK 180

181 GTGENYRCGNVAVTVSGHTCOHWSAOTPHTHERTPENFPCKNLDENYCRNPDGKRAPWCHT 240

181 GIGENIRGNVAVI VSGHICQWNSAQIFHHKREFFENTFCAGNDDENTCAGW DOUGCH HCH

RESULT 13

CC in inhibiting vascular leakage, inflammation and fibrosis in an
CC animal having diabetes, chronic inflammation, brain edema, arthritis,
CC uveitis, macular edema, cancer, hyperglycemia, a kidney inflammatory
CC disease, a disorder resulting in kidney fibrosis and/or a disorder of the
CC kidney resulting in proteinuria. The present sequence is the human
CC angiotensin protein.
XX
SQ

Sequence 339 NA;

Query Match	99.7%;	Score 1535;	DB 9;	Length 339;
Best Local Similarity	99.6%;	Pred. No. 2.8e-90;		
Matches 259;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	1	VYLSECKTGKNGYRGTMSKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN	60	
Db	1	VYLSECKTGKNGYRGTMSKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN	60	
QY	61	DQGPWCYTTDPKRYDYCDILLECEECMHCSGENYDGIKSKTMSGLECQAWDSQSPH	120	
Db	61	DQGPWCYTTDPKRYDYCDILLECEECMHCSGENYDGIKSKTMSGLECQAWDSQSPH	120	
QY	121	GYIPSPFNKLNKKNYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTTPPSSGPTYQCLK	180	
Db	121	GYIPSPFNKLNKKNYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTTPPSSGPTYQCLK	180	
QY	181	GTGENTRGNAVTVSGHTCOHWSAQTPTHTERTPENPCKNLDENYCRNPDGKRAPWCHT	240	
Db	181	GTGENTRGNAVTVSGHTCOHWSAQTPTHTERTPENPCKNLDENYCRNPDGKRAPWCHT	240	
QY	241	TNSQVWEYCKIPSCDSSPV	260	
Db	241	TNSQVWEYCKIPSCDSSPV	260	

Search completed: August 29, 2006, 13:56:10
Job time : 201 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 29, 2006, 14:14:04 ; Search time 33 Seconds
(without alignments)
539.087 Million cell updates/sec

Title: US-09-502-176-2

Perfect score: 1540

Sequence: 1 VYLSEKCTGNGNYRGTMASK.....TNSQVRWEYKIPSCDSSPV 260

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 247503 seqs, 68422524 residues

Total number of hits satisfying chosen parameters: 247503

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:

1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1537	99.8	869	US-10-503-836-35	Sequence 35, Appl
2	1537	99.8	869	US-10-503-836-37	Sequence 37, Appl
3	1535	99.7	791	US-11-318-939-6	Sequence 6, Appli
4	1519.5	98.7	790	US-11-350-703-1	Sequence 1, Appli
5	1442	93.6	810	US-11-318-939-11	Sequence 11, Appl
6	1292	83.9	790	US-11-318-939-13	Sequence 13, Appl
7	1291	83.8	812	US-11-318-939-7	Sequence 7, Appli
8	1274	82.7	812	US-11-318-939-12	Sequence 12, Appl
9	1237	80.3	809	US-11-318-939-9	Sequence 9, Appli
10	794	51.6	475	US-11-328-070-14	Sequence 14, Appl
11	794	51.6	482	US-11-328-070-13	Sequence 13, Appl
12	794	51.6	566	US-11-328-070-2	Sequence 2, Appli
13	309.5	20.1	562	US-10-505-928-547	Sequence 547, App
14	309.5	20.1	562	US-11-183-218-26	Sequence 26, Appl
15	279.5	18.1	333	US-11-318-939-8	Sequence 8, Appli
16	278.5	18.1	703	US-10-503-836-39	Sequence 39, Appl
17	278.5	18.1	703	US-10-503-836-41	Sequence 41, Appl
18	263	17.1	338	US-11-318-939-10	Sequence 10, Appl
19	188.5	12.2	655	US-11-242-617-1	Sequence 1, Appli
20	170.5	11.1	653	US-11-242-617-2	Sequence 2, Appli
21	164	10.6	476	US-11-264-088-1	Sequence 1, Appli
22	164	10.6	476	US-11-311-475-1	Sequence 1, Appli
23	156	10.1	264	US-11-191-457-2	Sequence 2, Appli
24	150	9.7	27	US-11-134-871-698	Sequence 698, App
25	142	9.2	263	US-11-191-457-4	Sequence 4, Appli

26	135	8.8	431	6	US-10-505-928-465	Sequence 465, App
27	135	8.8	431	7	US-11-183-218-34	Sequence 34, Appl
28	135	8.8	477	7	US-11-264-088-2	Sequence 2, Appli
29	135	8.8	477	7	US-11-311-475-2	Sequence 2, Appli
30	134	8.7	138	7	US-11-330-353-12	Sequence 12, Appl
31	108	7.0	663	7	US-11-290-896-24	Sequence 24, Appl
32	106	6.9	685	7	US-11-175-714-2	Sequence 2, Appli
33	106	6.9	685	7	US-11-175-714-28	Sequence 28, Appl
34	106	6.9	685	7	US-11-175-714-32	Sequence 32, Appl
35	106	6.9	685	7	US-11-175-714-34	Sequence 34, Appl
36	106	6.9	685	7	US-11-175-714-36	Sequence 36, Appl
37	106	6.9	685	7	US-11-175-714-38	Sequence 38, Appl
38	106	6.9	685	7	US-11-178-724-20	Sequence 20, Appl
39	106	6.9	685	7	US-11-264-243-2	Sequence 2, Appli
40	106	6.9	685	7	US-11-071-796A-19	Sequence 19, Appl
41	105.5	6.9	429	7	US-11-290-896-40	Sequence 40, Appl
42	105.5	6.9	631	7	US-11-290-896-25	Sequence 25, Appl
43	104.5	6.8	2556	7	US-11-264-243-6	Sequence 6, Appli
44	102.5	6.7	2556	7	US-11-071-796A-22	Sequence 22, Appl
45	98.5	6.4	1953	7	US-11-264-243-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1

US-10-503-836-35
; Sequence 35, Application US/10503836
; Publication No. US20060122374A1

GENERAL INFORMATION:
; APPLICANT: Mertins, Peter

; APPLICANT: Celik, Ilhan

; APPLICANT: Kisker, Oliver

; APPLICANT: Sleep, Darrell

; APPLICANT: Hay, Joanna

; APPLICANT: Hauser, Hans-Peter

; TITLE OF INVENTION: ALBUMIN FUSED ANTI-ANGIOGENESIS PEPTIDES

; FILE REFERENCE: P27,972 USA

; CURRENT APPLICATION NUMBER: US/10/503,836

; CURRENT FILING DATE: 2004-08-06

; PRIOR APPLICATION NUMBER: PCT/IB03/00433

; PRIOR FILING DATE: 2003-02-07

; PRIOR APPLICATION NUMBER: 60/355,547

; PRIOR FILING DATE: 2002-02-07

; NUMBER OF SEQ ID NOS: 47

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 35

; LENGTH: 869

; TYPE: PPT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Amino acid sequence of the N-terminal angiotensin (non glycosylated) - albumin fusion protein

US-10-503-836-35

Query Match 99.8%; Score 1537; DB 6; Length 869;

Best Local Similarity 99.6%; Pred. No. 2.3e-120;

Matches 259; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1	VYLSEKCTGNGNYRGTMASKNGITCQKWSSTSPHPRFSPATHPSGLLENYCRNPDN	60
Db	25	VYLSEKCTGNGNYRGTMASKNGITCQKWSSTSPHPRFSPATHPSGLLENYCRNPDN	84
QY	61	DPQGPWCYTTDEPKRYDYCDILLECEECMHCSGENYDGKISKTMGLGCOAWDSQSPH	120
Db	85	DPQGPWCYTTDEPKRYDYCDILLECEECMHCSGENYDGKISKTMGLGCOAWDSQSPH	144
QY	121	GYIPSPFPNNKLNKNCYCRNPDRPWCFTTDPNKKWELCDIPRCTPPSPSSGFTQCLK	180
Db	145	GYIPSPFPNNKLNKNCYCRNPDRPWCFTTDPNKKWELCDIPRCTPPSPSSGFTQCLK	204
QY	181	GTGENTRGVAVTVSGHTCOHSAQTPHTRPENPCKNLDENYCRNPDGKRAPWCHT	240

Db 205 GTGENYRGNAVTVSGHTCQHSQAOTPHTHQRTPEFPCCKNLNDENYCRNPDGKRAPWCHT 264

QY 241 TNSQVRWEYCKIPSCDSSPV 260

Db 265 TNSQVRWEYCKIPSCDSSPV 284

RESULT 2

US-10-503-836-37

Sequence 37, Application US/10503836

Publication No. US20060122374A1

GENERAL INFORMATION:

APPLICANT: Mertins, Peter

APPLICANT: Celik, Ilhan

APPLICANT: Kisker, Oliver

APPLICANT: Sleep, Darrell

APPLICANT: Hay, Joanna

APPLICANT: Hauser, Hans-Peter

TITLE OF INVENTION: ALBUMIN FUSED ANTI-ANGIOGENESIS PEPTIDES

FILE REFERENCE: P27,972 USA

CURRENT APPLICATION NUMBER: US/10/503,836

CURRENT FILING DATE: 2004-08-06

PRIOR APPLICATION NUMBER: PCT/IB03/00433

PRIOR FILING DATE: 2003-02-07

PRIOR APPLICATION NUMBER: 60/355,547

PRIOR FILING DATE: 2002-02-07

NUMBER OF SEQ ID NOS: 47

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 37

LENGTH: 869

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

* OTHER INFORMATION: Description of Artificial Sequence: Amino acid sequence at the C-terminal of albumin angiotensin (non glycosylated) - fusion protein

US-10-503-836-37

Query Match 99.8%; Score 1537; DB 6; Length 869;

Best Local Similarity 99.6%; Pred. No. 2.3e-120;

Matches 259; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGYRTGSKTNGITCQKWSSTSPHRPFSPTATHPSEGLEENYCRNPDN 60

Db 610 VYLSECKTGNGKNGYRTGSKTNGITCQKWSSTSPHRPFSPTATHPSEGLEENYCRNPDN 669

QY 61 DPQGPWCYTTDPEKRYDYCDILLECEECMHCSENGYDGIKSTMSGLECQAWDSQSPH 120

Db 670 DPQGPWCYTTDPEKRYDYCDILLECEECMHCSENGYDGIKSTMSGLECQAWDSQSPH 729

QY 121 GYIPSKFPNKLKNGYCRNPDRELPCWCTTDPNKRWELCDIPRCTTPPSSGPTYQCLK 180

Db 730 GYIPSKFPNKLKNGYCRNPDRELPCWCTTDPNKRWELCDIPRCTTPPSSGPTYQCLK 789

QY 181 GTGENYRGNAVTVSGHTCQHSQAOTPHTHQRTPEFPCCKNLNDENYCRNPDGKRAPWCHT 240

Db 790 GTGENYRGNAVTVSGHTCQHSQAOTPHTHQRTPEFPCCKNLNDENYCRNPDGKRAPWCHT 849

QY 241 TNSQVRWEYCKIPSCDSSPV 260

Db 850 TNSQVRWEYCKIPSCDSSPV 869

RESULT 3

US-11-318-939-6

Sequence 6, Application US/11318939

Publication No. US20060099671A1

GENERAL INFORMATION:

APPLICANT: Soff, Gerald

APPLICANT: Gately, Stephen T.

APPLICANT: Twardowski, Przemyslaw

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR GENERATING ANGIOSTATIN

FILE REFERENCE: 4228-1-1-1

CURRENT APPLICATION NUMBER: US/11/318,939

QY 1 VYLSECKTGNGKNGYRTGSKTNGITCQKWSSTSPHRPFSPTATHPSEGLEENYCRNPDN 60

Db 79 VYLSECKTGNGKNGYRTGSKTNGITCQKWSSTSPHRPFSPTATHPSEGLEENYCRNPDN 138

QY 61 DPQGPWCYTTDPEKRYDYCDILLECEECMHCSENGYDGIKSTMSGLECQAWDSQSPH 120

Db 139 DPQGPWCYTTDPEKRYDYCDILLECEECMHCSENGYDGIKSTMSGLECQAWDSQSPH 198

QY 121 GYIPSKFPNKLKNGYCRNPDRELPCWCTTDPNKRWELCDIPRCTTPPSSGPTYQCLK 180

Db 199 GYIPSKFPNKLKNGYCRNPDRELPCWCTTDPNKRWELCDIPRCTTPPSSGPTYQCLK 258

QY 181 GTGENYRGNAVTVSGHTCQHSQAOTPHTHQRTPEFPCCKNLNDENYCRNPDGKRAPWCHT 240

Db 259 GTGENYRGNAVTVSGHTCQHSQAOTPHTHQRTPEFPCCKNLNDENYCRNPDGKRAPWCHT 318

QY 241 TNSQVRWEYCKIPSCDSSPV 260

Db 319 TNSQVRWEYCKIPSCDSSPV 338

RESULT 4

US-11-350-703-1

Sequence 1, Application US/11350703

Publication No. US20060135428A1

GENERAL INFORMATION:

APPLICANT: Bridon, Dominique P.

APPLICANT: Rasamoeliso, Michele

APPLICANT: Thibaudau, Karen

APPLICANT: Huang, Xicai

APPLICANT: Bellevue, Richard

TITLE OF INVENTION: LONG LASTING ANTI-ANGIOGENIC PEPTIDES

FILE REFERENCE: 500862001401

CURRENT APPLICATION NUMBER: US/11/350,703

CURRENT FILING DATE: 2006-02-08

PRIOR APPLICATION NUMBER: US 09/623,543

PRIOR FILING DATE: 2000-09-05

PRIOR APPLICATION NUMBER: PCT/IB00/00763

PRIOR FILING DATE: 2000-05-17

PRIOR APPLICATION NUMBER: 60/134,406

PRIOR FILING DATE: 1999-05-17

PRIOR APPLICATION NUMBER: 09/657,431

PRIOR FILING DATE: 2000-09-07

PRIOR APPLICATION NUMBER: 60/153,406

PRIOR FILING DATE: 1999-09-10

PRIOR APPLICATION NUMBER: 60/159,783

PRIOR FILING DATE: 1999-10-15

NUMBER OF SEQ ID NOS: 67

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1

LENGTH: 790

TYPE: PRT

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Peptide
US-11-350-703-1

Query Match 98.7%; Score 1519.5; DB 7; Length 790;
Best Local Similarity 99.2%; Pred. No. 6e-119;
Matches 258; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 VYLSECKTGNGKNGYRTGSKTNGITCQKWSSTSPHPRFSPATHPSEGLEENYCRNPDN 60
DB 79 VYLSECKTGNGKNGYRTGSKTNGITCQKWSSTSPHPRFSPATHPSEGLEENYCRNPDN 137
QY 61 DPQGPWCYTTDPKRYDYCDILECEBECMHCSENGYDGIKSKTMSGLECOAWDSQSPHAH 120
DB 138 DPQGPWCYTTDPKRYDYCDILECEBECMHCSENGYDGIKSKTMSGLECOAWDSQSPHAH 197
QY 121 GYIPSKFPNKLKKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTPPPSSGPTYQCLK 180
DB 198 GYIPSKFPNKLKKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTPPPSSGPTYQCLK 257
QY 181 GTGENYRGNAVTVSGHTCOHWSAQTPTHTERTPENFPCKNLNDENYCRNPDGKRAPWCHT 240
DB 258 GTGENYRGNAVTVSGHTCOHWSAQTPTHTERTPENFPCKNLNDENYCRNPDGKRAPWCHT 317
QY 241 TNSQVRWEYCKIPSCDSSPV 260
DB 318 TNSQVRWEYCKIPSCDSSPV 337

RESULT 5

US-11-318-939-11

Sequence 11, Application US/11318939
Publication No. US20060099671A1
GENERAL INFORMATION:
APPLICANT: Gately, Stephen T.
APPLICANT: Twardowski, Przemyslaw
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR GENERATING ANGIOSTATIN
FILE REFERENCE: 4228-1-1-1
CURRENT FILING DATE: 2005-12-22
PRIOR FILING DATE: 2000-02-08
PRIOR APPLICATION NUMBER: US/09/500,397
PRIOR FILING DATE: 1996-09-17
PRIOR FILING DATE: 1996-09-17
PRIOR FILING DATE: 1997-12-15
PRIOR FILING DATE: 1997-12-15
PRIOR FILING DATE: 1997-09-17
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 11
LENGTH: 810
TYPE: PRT
ORGANISM: Macaca mulatta
US-11-318-939-11

Query Match 93.6%; Score 1442; DB 7; Length 810;
Best Local Similarity 93.1%; Pred. No. 1.8e-112;
Matches 242; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGYRTGSKTNGITCQKWSSTSPHPRFSPATHPSEGLEENYCRNPDN 60
DB 98 VYLSECKTGNGKNGYRTGSKTNGITCQKWSSTSPHPRFSPATHPSEGLEENYCRNPDN 157
QY 61 DPQGPWCYTTDPKRYDYCDILECEBECMHCSENGYDGIKSKTMSGLECOAWDSQSPHAH 120
DB 158 DPQGPWCYTTDPKRYDYCDILECEBECMHCSENGYDGIKSKTMSGLECOAWDSQSPHAH 217
QY 121 GYIPSKFPNKLKKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTPPPSSGPTYQCLK 180
DB 218 GYIPSKFPNKLKKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTPPPSSGPTYQCLK 277

QY 181 GTGENYRGNAVTVSGHTCOHWSAQTPTHTERTPENFPCKNLNDENYCRNPDGKRAPWCHT 240
DB 278 GTGENYRGNAVTVSGHTCHGWSAQTPTHTERTPENFPCKNLNDENYCRNPDGKRAPWCHT 337
QY 241 TNSQVRWEYCKIPSCDSSPV 260
DB 338 TNSQVRWEYCKIPSCDSSPV 357

RESULT 6

US-11-318-939-13
Sequence 13, Application US/11318939
Publication No. US20060099671A1
GENERAL INFORMATION:
APPLICANT: Soff, Gerald
APPLICANT: Gately, Stephen T.
APPLICANT: Twardowski, Przemyslaw
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR GENERATING ANGIOSTATIN
FILE REFERENCE: 4228-1-1-1
CURRENT FILING DATE: 2005-12-22
PRIOR FILING DATE: 2000-02-08
PRIOR APPLICATION NUMBER: US/09/500,397
PRIOR FILING DATE: 1996-09-17
PRIOR FILING DATE: 1996-09-17
PRIOR FILING DATE: 1997-12-15
PRIOR FILING DATE: 1997-12-15
PRIOR FILING DATE: 1997-09-17
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 13
LENGTH: 790
TYPE: PRT
ORGANISM: Sus scrofa
US-11-318-939-13

Query Match 83.9%; Score 1292; DB 7; Length 790;

Best Local Similarity 81.4%; Pred. No. 5.6e-100;
Matches 210; Conservative 23; Mismatches 25; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGYRTGSKTNGITCQKWSSTSPHPRFSPATHPSEGLEENYCRNPDN 60
DB 79 VYLSECKTGNGKNGYRTGSKTNGITCQKWSSTSPHPRFSPATHPSEGLEENYCRNPDN 138
QY 61 DPQGPWCYTTDPKRYDYCDILECEBECMHCSENGYDGIKSKTMSGLECOAWDSQSPHAH 120
DB 139 DEKGPWCYTTDPKRYDYCDILECEBECMHCSENGYDGIKSKTMSGLECOAWDSQSPHAH 198
QY 121 GYIPSKFPNKLKKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTPPPSSGPTYQCLK 180
DB 199 GYIPSKFPNKLKKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTPPPSSGPTYQCLK 258
QY 181 GTGENYRGNAVTVSGHTCOHWSAQTPTHTERTPENFPCKNLNDENYCRNPDGKRAPWCHT 240
DB 259 GTGENYRGNAVTVSGHTCOHWSAQTPTHTERTPENFPCKNLNDENYCRNPDGKRAPWCHT 318
QY 241 TNSQVRWEYCKIPSCDSSPV 258
DB 319 TNSQVRWEYCKIPSCDSSPV 336

RESULT 7

US-11-318-939-7
Sequence 7, Application US/11318939
Publication No. US20060099671A1
GENERAL INFORMATION:
APPLICANT: Soff, Gerald
APPLICANT: Gately, Stephen T.
APPLICANT: Twardowski, Przemyslaw
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR GENERATING ANGIOSTATIN
FILE REFERENCE: 4228-1-1-1

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; CURRENT APPLICATION NUMBER: US/11/318,939
; CURRENT FILING DATE: 2005-12-22
; PRIOR APPLICATION NUMBER: US/09/500,397
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/710,305
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-09-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/991,761
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-15
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US97/16539
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-17
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 812
; TYPE: PRT
; ORGANISM: Bos taurus
; US-11-318-939-7

Query Match      83.8%; Score 1291; DB 7; Length 812;
Best Local Similarity 80.8%; Pred. No. 6.9e-100;
Matches 210; Conservative 23; Mismatches 27; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNYRGTMSTKNGITCQKWSSTSPHRPFSATHPSSEGLEENYCRNPDN 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 105 IYLECKTGNGQYRGTTAETKSGVTCQKWSATSPHVKPSPEKPLAGLEENYCRNPDN 164
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 DQGPWCYTTDPKRYDYCDILECEECWCHSCGENYDGIKISKTMSGLECQAWDSQSPHAAH 120
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 165 DENGWCYTTDPKRYDYCDIPECEDKCHSCGENYEGKIAKTMSGRDCQAWDSQSPHAAH 224
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 121 GYIPSKFPNNKLNKYNCRNPDRPLPWCFTTDPNKRWELCDIPRCTTTPPSSGPTYQCLK 180
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 225 GYIPSKFPNNKLNKYNCRNPDRPWCFTTDPQKRWECFDPRCTTTPPSSGPTYQCLK 284
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 181 GTGENYRGNVAVTVSGHTCOHWSAQTPTHTERTPENFCKNLNDENYCRNPDGKRAPWCHT 240
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 285 GTGKNYGGTVAVTESGHTCQWSEQTPHRHNRTPENFCKNLNDENYCRNPNGEKAPWCYT 344
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 241 TNSQVRWEYCKIPSCDSSPV 260
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 345 TNSQVRWEYCKIPSCDSSPL 364
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 8
US-11-318-939-12
; Sequence 12, Application US/11318939
; Publication NO. US20060099671A1
; GENERAL INFORMATION:
; APPLICANT: Gately, Stephen T.
; APPLICANT: Twardowski, Przemyslaw
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR GENERATING ANGIOSTATIN
; FILE REFERENCE: 4228-1-1-1
; CURRENT APPLICATION NUMBER: US/11/318,939
; CURRENT FILING DATE: 2005-12-22
; PRIOR APPLICATION NUMBER: US/09/500,397
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/710,305
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-09-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/991,761
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-15
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US97/16539
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-17
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; TYPE: PRT
; ORGANISM: Mus musculus
; US-11-318-939-12

Query Match      82.7%; Score 1274; DB 7; Length 812;
Best Local Similarity 80.6%; Pred. No. 1.8e-98;
Matches 201; Conservative 26; Mismatches 31; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNYRGTMSTKNGITCQKWSSTSPHRPFSATHPSSEGLEENYCRNPDN 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 98 MYLSECKGVNGKYRGTVGTSKNGITCQKWSATPHKPRFSPDENPSEGLDQNYCRNPDN 157
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 DQGPWCYTTDPKRYDYCDILECEECWCHSCGENYDGIKISKTMSGLECQAWDSQSPHAAH 120
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 158 DPKGWCYTMDEPVEYECIIQCEDECHSCGQYVVKISRTMSGLECQAWDSQSPHAAH 217
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 121 GYIPSKFPNNKLNKYNCRNPDRPLPWCFTTDPNKRWELCDIPRCTTTPPSSGPTYQCLK 180
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 218 GFIPSKFPNNKLNKYNCRNPDRPWCFTTMDNRKWEYCDIPRCTTTPPSSGPTYQCLK 277
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 181 GTGENYRGNVAVTVSGHTCOHWSAQTPTHTERTPENFCKNLNDENYCRNPDGKRAPWCHT 240
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 278 GNGHYQGNVAVTVSGLTQCRWGEQSPHRHDKRPENYPCKNLDENYCRNPDGEPAPWCT 337
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 241 TNSQVRWEYCKIPSCDSS 258
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
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Db 338 TNSVRWFCKIPDCVSS 355

RESULT 10
US-11-328-070-14
; Sequence 14, Application US/11328070
; Publication No. US20060104964A1
; GENERAL INFORMATION:
; APPLICANT: JIANG, WEN G.
; TITLE OF INVENTION: RECOMBINANT SEQUENCE, ITS PREPARATION AND USE
; FILE REFERENCE: 3007-1017
; CURRENT APPLICATION NUMBER: US/11/328,070
; CURRENT FILING DATE: 2006-01-10
; PRIOR APPLICATION NUMBER: PCT/GB01/01956
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: GB 0010630.2
; PRIOR FILING DATE: 2000-05-04
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-328-070-14

Query Match	51.6%	Score	794	DB	7	Length	475
Best Local Similarity	50.2%	Pred. No.	1.1e-58				
Matches	133	Conservative	41	Mismatches	81	Indels	10
Gaps	4						
QY	2	YLSECKTGNGKNGYGTWSTKNGTTCCKWASTSPHRRPESPATPHSGLEGRNYCNRPNDD	61				
DB	121	YIRNCIIIGRSYKGTYSITKSGIKCQPSWMIPEHSFLPSSYRGKDLQENYCNRPGE	180				
QY	62	POGFWCYTTDPKRYDYCDILECEE-EOMCGSGENYDGKISKTWMSGLECQAWDSQSPHAX	120				
DB	181	EGGPFWCFTSNPEVRYEYCDIPQCSEVECWTCNGESYRGLMDHTBESGKICQAWDHQTTPRH	240				
QY	121	GYLPSKFPNNLKNKYCNRNPDRELPRWCFTTDPNKRWELCDIPRCT-----TPPSSGP	174				
DB	241	KFLPERYPDKGDDNYCNRNPDQGRPPWCYTLDPHRWEYCAIKTCANTVNDTDPME--	298				
QY	175	TYOCLKGTGNYRGNAVTVTSGHTCQHWSAQTPHTHRTPENPFCKNLDENYCNPNQGR	234				
DB	299	TTETCICQGGSGYRGNTANTWNGIPCQRWDSQYPHKHDWTPENPFCKDLRENYCNRPDGSE	358				

```

235 APCHTTNSQRMWEYC-KIPSCDSS 258
:|:|:|:|:|:|:|:|:|:|:|:|:|
359 SPWCFTDPNIRVGYCQIPNCMDWS 383

RESULT 11
US-11-328-070-13
; Sequence 13, Application US/11328070
; Publication No. US20060104964A1
; GENERAL INFORMATION:
; APPLICANT: JIANG, WEN G.
; TITLE OF INVENTION: RECOMBINANT SEQUENCE, ITS PREPARATION AND USE
; FILE REFERENCE: 3007-1017
; CURRENT APPLICATION NUMBER: US/11/328,070
; CURRENT FILING DATE: 2006-01-10
; PRIOR APPLICATION NUMBER: PCT/GB01/01956
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: GB 0010630.2
; PRIOR FILING DATE: 2000-05-04
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 482
; TYPE: PRT

```

CS-11-328-070-13

```

; Sequence 547, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 547
; LENGTH: 562
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-547

Query Match      20.1%; Score 309.5; DB 6; Length 562;
Best Local Similarity 34.1%; Pred. No. 3.2e-18;
Matches 77; Conservative 23; Mismatches 103; Indels 23; Gaps 9;

QY 46 PSEGLEENYCRNPDNDPQGWPCYTTD-----PEKRYDYCDILECEBECMHCSGENYDGKI 100
DB 82 PVKSCSEPRCFNGGTCQQA--LYFSDFVQCPEGFAGKCCBIDTRATCYEDQGISYRGTW 139
QY 101 SKTMSGLECAQWDS---QSPHAGHYIPSKFNNKLNKKNYCRNPDRELPRWCFTTDPNK- 155
DB 140 STAESGAECTNNWSSALAQKPYSGRRPDAILGLGNHNYCRNPDRLSDKPCWCVFVFKAGY 198
QY 156 RWELCDIPRCTTPPPSSGGTYCQLKGTGENYGNVAVTVSGHTCQHWSAQTPHTHRTTPE 215
DB 199 SSEFCSTPAC-----SEGNS-DCYFGNGSAYRGTHSLTSGASCLPWNMILIGKYVTTAQ 252
QY 216 NPFCKNL-----DENYCRNPDGKRAPWCHT--TNSQVRWEYCKIPSCDS 257
DB 253 NPSAQAALGLGKHNKYNCRNPDGDAKPCWCHVLKNRRLTWECYDCVPSCSST 298

RESULT 14
US-11-183-218-26
; Sequence 26, Application US/11183218
; Publication No. US20060088906A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Catyne
; TITLE OF INVENTION: ERYTHROPOIETIN: REMODELING AND
; TITLE OF INVENTION: GLYCOCONJUGATION OF ERYTHROPOIETIN
; FILE REFERENCE: 040853-01-5083-US02
; CURRENT APPLICATION NUMBER: US/11/183,218
; CURRENT FILING DATE: 2005-07-15
; PRIOR APPLICATION NUMBER: US 10/410,945
; PRIOR FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: PCT/US02/32263
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US 60/334,301

; Sequence 547, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 547
; LENGTH: 562
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-547

Query Match      20.1%; Score 309.5; DB 6; Length 562;
Best Local Similarity 34.1%; Pred. No. 3.2e-18;
Matches 77; Conservative 23; Mismatches 103; Indels 23; Gaps 9;

QY 46 PSEGLEENYCRNPDNDPQGWPCYTTD-----PEKRYDYCDILECEBECMHCSGENYDGKI 100
DB 82 PVKSCSEPRCFNGGTCQQA--LYFSDFVQCPEGFAGKCCBIDTRATCYEDQGISYRGTW 139
QY 101 SKTMSGLECAQWDS---QSPHAGHYIPSKFNNKLNKKNYCRNPDRELPRWCFTTDPNK- 155
DB 140 STAESGAECTNNWSSALAQKPYSGRRPDAILGLGNHNYCRNPDRLSDKPCWCVFVFKAGY 198
QY 156 RWELCDIPRCTTPPPSSGGTYCQLKGTGENYGNVAVTVSGHTCQHWSAQTPHTHRTTPE 215
DB 199 SSEFCSTPAC-----SEGNS-DCYFGNGSAYRGTHSLTSGASCLPWNMILIGKYVTTAQ 252
QY 216 NPFCKNL-----DENYCRNPDGKRAPWCHT--TNSQVRWEYCKIPSCDS 257
DB 253 NPSAQAALGLGKHNKYNCRNPDGDAKPCWCHVLKNRRLTWECYDCVPSCSST 298

RESULT 15
US-11-318-939-8
; Sequence 8, Application US/11318939
; Publication No. US20060099671A1
; GENERAL INFORMATION:
; APPLICANT: Soff, Gerald
; APPLICANT: Gately, Stephen T.
; APPLICANT: Twardowski, Przemyslaw
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR GENERATING ANGIOSTATIN
; FILE REFERENCE: 4228-1-1-1
; CURRENT APPLICATION NUMBER: US/11/318,939
; CURRENT FILING DATE: 2005-12-22
; PRIOR APPLICATION NUMBER: US/09/500,397
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/710,305
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-09-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/991,761
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-15
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US97/16539
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-17
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Canis familiaris
US-11-318-939-8

Query Match      18.1%; Score 279.5; DB 7; Length 333;
Best Local Similarity 48.5%; Pred. No. 5.8e-16;
Matches 47; Conservative 13; Mismatches 36; Indels 1; Gaps 1;

QY 4 SECKTNGKNGYRTGMSKTKNGITCKQWSSTSPHRPR-FSPATHPSGLEENYCRNPDNDP 62
DB 2 SDCMFGNGKGYGKKATTVMGIPCCQEWAAQEPHRHSIFTPETNPQAGLEKKNYCRNPDGDV 61
QY 63 QGPWCYTTDPEKRYDYCDILECEBECMHCSGENYDGK 99
DB 62 NGFWCYTWNQRKLFYDCVPCVSTSFDCGKQVPEPK 98

```

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; Sequence 547, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 547
; LENGTH: 562
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-547

Query Match      20.1%; Score 309.5; DB 6; Length 562;
Best Local Similarity 34.1%; Pred. No. 3.2e-18;
Matches 77; Conservative 23; Mismatches 103; Indels 23; Gaps 9;

QY 46 PSEGLEENYCRNPDNDPQGWPCYTTD-----PEKRYDYCDILECEBECMHCSGENYDGKI 100
DB 82 PVKSCSEPRCFNGGTCQQA--LYFSDFVQCPEGFAGKCCBIDTRATCYEDQGISYRGTW 139
QY 101 SKTMSGLECAQWDS---QSPHAHGVIKPKFNKLNKKNYCRNPDRELPRWCFTTDPNK- 155
DB 140 STAESGAECTNWNSSALAKQPKYS-GRPDARILGLGNHNYCRNPDRLSDKPCWCVFVFKAGY 198
QY 156 RWELCDIPRCTTPPPSSGGTYCQLKGTGENYGNVAVTVSGHTCQHWSAQTPHTHRTTPE 215
DB 199 SSEFCSTPAC-----SEGNS-DCYFGNGSAYRGTHSLTSGASCLPWNMILIGKVYTAQ 252
QY 216 NPFCKNL----DENYCRNPDGKRAPWCHT--TNSQVRWEYCKIPSCDS 257
DB 253 NPSAQAALGLGKHNYCRNPDGDAKWPCHVILKNRRLTWECYDCVPSCSST 298

RESULT 14
US-11-183-218-26
; Sequence 26, Application US/11183218
; Publication No. US20060088906A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Catyne
; TITLE OF INVENTION: ERYTHROPOIETIN: REMODELING AND
; TITLE OF INVENTION: GLYCOCONJUGATION OF ERYTHROPOIETIN
; FILE REFERENCE: 040853-01-5083-US02
; CURRENT APPLICATION NUMBER: US/11/183,218
; CURRENT FILING DATE: 2005-07-15
; PRIOR APPLICATION NUMBER: US 10/410,945
; PRIOR FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: PCT/US02/32263
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US 60/334,301

; Sequence 547, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 547
; LENGTH: 562
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-547

Query Match      20.1%; Score 309.5; DB 6; Length 562;
Best Local Similarity 34.1%; Pred. No. 3.2e-18;
Matches 77; Conservative 23; Mismatches 103; Indels 23; Gaps 9;

QY 46 PSEGLEENYCRNPDNDPQGWPCYTTD-----PEKRYDYCDILECEBECMHCSGENYDGKI 100
DB 82 PVKSCSEPRCFNGGTCQQA--LYFSDFVQCPEGFAGKCCBIDTRATCYEDQGISYRGTW 139
QY 101 SKTMSGLECAQWDS---QSPHAHGVIKPKFNKLNKKNYCRNPDRELPRWCFTTDPNK- 155
DB 140 STAESGAECTNWNSSALAKQPKYS-GRPDARILGLGNHNYCRNPDRLSDKPCWCVFVFKAGY 198
QY 156 RWELCDIPRCTTPPPSSGGTYCQLKGTGENYGNVAVTVSGHTCQHWSAQTPHTHRTTPE 215
DB 199 SSEFCSTPAC-----SEGNS-DCYFGNGSAYRGTHSLTSGASCLPWNMILIGKVYTAQ 252
QY 216 NPFCKNL----DENYCRNPDGKRAPWCHT--TNSQVRWEYCKIPSCDS 257
DB 253 NPSAQAALGLGKHNYCRNPDGDAKWPCHVILKNRRLTWECYDCVPSCSST 298

RESULT 15
US-11-318-939-8
; Sequence 8, Application US/11318939
; Publication No. US20060099671A1
; GENERAL INFORMATION:
; APPLICANT: Soff, Gerald
; APPLICANT: Gately, Stephen T.
; APPLICANT: Twardowski, Przemyslaw
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR GENERATING ANGIOSTATIN
; FILE REFERENCE: 4228-1-1-1
; CURRENT APPLICATION NUMBER: US/11/318,939
; CURRENT FILING DATE: 2005-12-22
; PRIOR APPLICATION NUMBER: US/09/500,397
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/710,305
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-09-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/991,761
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-15
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US97/16539
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-17
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Canis familiaris
US-11-318-939-8

Query Match      18.1%; Score 279.5; DB 7; Length 333;
Best Local Similarity 48.5%; Pred. No. 5.8e-16;
Matches 47; Conservative 13; Mismatches 36; Indels 1; Gaps 1;

QY 4 SECKTGNKGYRTGWSKTKNGITCKQWSSTSPHRPR-FSPATHPSGLEENYCRNPDNDP 62
DB 2 SDCMFGNGKGYRGKATTVMGIPCCQEWAAQEPHRHSIFTPETNPQAGLEKKNYCRNPDGDV 61
QY 63 QGPWCYTTDPEKRYDYCDILECEBECMHCSGENYDGK 99
DB 62 NGFWCYTWNQRKLFYDCVPCVSTSFDCGKQVPEPK 98

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Search completed: August 29, 2006, 14:17:35
Job time : 34 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 29, 2006, 14:13:24 ; Search time 181 Seconds

(without alignments)
665.392 Million cell updates/sec

Title: US-09-502-176-2

Perfect score: 1540

Sequence: 1 VYLSECKTGNGKNGYRTWSK.....TNSQVRWEYCKIPSCDSSPV 260

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1540	100.0	260	4	US-10-131-241-61
2	1535	99.7	303	5	US-10-810-262-11
3	1535	99.7	339	3	US-09-788-142-3
4	1535	99.7	339	3	US-09-761-120-3
5	1535	99.7	339	3	US-09-335-325-3
6	1535	99.7	339	4	US-10-131-241-3
7	1535	99.7	339	4	US-10-127-066-3
8	1535	99.7	339	4	US-10-402-364-3
9	1535	99.7	339	4	US-10-401-108-3
10	1535	99.7	339	6	US-11-010-874-3
11	1535	99.7	378	3	US-10-292-418-11
12	1535	99.7	378	3	US-09-873-676-1
13	1535	99.7	378	3	US-09-335-325-42
14	1535	99.7	378	4	US-10-131-241-42
15	1535	99.7	378	4	US-10-127-066-42
16	1535	99.7	391	4	US-10-304-287-7
17	1535	99.7	391	4	US-10-415-012-1
18	1535	99.7	391	4	US-10-735-577-7
19	1535	99.7	394	4	US-10-304-287-8
20	1535	99.7	394	4	US-10-415-012-2
21	1535	99.7	394	4	US-10-735-577-8
22	1535	99.7	484	4	US-10-135-872B-7
23	1535	99.7	567	4	US-10-741-601-413
24	1535	99.7	567	5	US-10-995-561-764
25	1535	99.7	569	3	US-09-946-893-5
26	1535	99.7	571	3	US-09-946-893-8
27	1535	99.7	576	3	US-09-946-893-6

28	1535	99.7	579	4	US-10-449-609-7	Sequence 7, Appli
29	1535	99.7	714	4	US-10-415-012-8	Sequence 8, Appli
30	1535	99.7	714	5	US-10-503-910-18	Sequence 18, Appli
31	1535	99.7	791	3	US-09-967-386-1	Sequence 1, Appli
32	1535	99.7	791	4	US-10-304-287-1	Sequence 1, Appli
33	1535	99.7	791	4	US-10-360-101-257	Sequence 257, App
34	1535	99.7	791	4	US-10-778-423-1	Sequence 1, Appli
35	1535	99.7	791	4	US-10-753-646-1	Sequence 1, Appli
36	1535	99.7	791	4	US-10-735-577-1	Sequence 1, Appli
37	1535	99.7	791	5	US-10-729-475-10	Sequence 10, Appli
38	1535	99.7	791	5	US-10-503-910-17	Sequence 17, Appli
39	1535	99.7	791	6	US-11-056-621-4	Sequence 4, Appli
40	1535	99.7	798	6	US-11-108-459-8	Sequence 8, Appli
41	1535	99.7	799	5	US-10-503-910-8	Sequence 8, Appli
42	1535	99.7	803	5	US-10-503-910-10	Sequence 10, Appli
43	1535	99.7	810	3	US-09-946-893-2	Sequence 2, Appli
44	1535	99.7	810	4	US-10-193-656-2	Sequence 2, Appli
45	1535	99.7	810	4	US-10-237-144-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-10-131-241-61

; Sequence 61, Application US/10131241

; Publication No. US20030012792A1

; GENERAL INFORMATION:

; APPLICANT: Holaday, John W.

; TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer

; TITLE OF INVENTION: and Regulating Angiogenesis Using Cancer Markers

; FILE REFERENCE: 05213-0344 43170-271565

; CURRENT APPLICATION NUMBER: US/10/131,241

; PRIOR FILING DATE: 2002-07-22

; PRIOR APPLICATION NUMBER: US 09/413,049

; PRIOR FILING DATE: 1999-10-06

; PRIOR APPLICATION NUMBER: US 09/316,802

; PRIOR FILING DATE: 1999-05-21

; PRIOR APPLICATION NUMBER: US 60/086,586

; PRIOR FILING DATE: 1998-05-22

; NUMBER OF SEQ ID NOS: 65

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 61

; LENGTH: 260

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-131-241-61

Query Match 100.0%; Score 1540; DB 4; Length 260;
Best Local Similarity 100.0%; Pred. No. 2.3e-120;
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	VYLSECKTGNGKNGYRTWSKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN	60
Db	1	VYLSECKTGNGKNGYRTWSKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN	60
QY	61	DQGGFWCYTTDPKRYDYCDILECEECHNCGSENYDGKISKTMSGLECQAWDSQSPHAH	120
Db	61	DQGGFWCYTTDPKRYDYCDILECEECHNCGSENYDGKISKTMSGLECQAWDSQSPHAH	120
QY	121	GYIPSKFPNKLKNGYCRNPDRELAPWCCTTDPNKRWELCDIPRCTTPPPSSGTYQCLK	180
Db	121	GYIPSKFPNKLKNGYCRNPDRELAPWCCTTDPNKRWELCDIPRCTTPPPSSGTYQCLK	180
QY	181	GTGYNRGNAVTVSGHTCOHWSAOTPHTHRTPEFPCKNLNDENYCRNPDGGRAPWCHT	240
Db	181	GTGYNRGNAVTVSGHTCOHWSAOTPHTHRTPEFPCKNLNDENYCRNPDGGRAPWCHT	240
QY	241	TNSQVRWEYCKIPSCDSSPV 260	
Db	241	TNSQVRWEYCKIPSCDSSPV 260	

RESULT 2

US-10-810-262-11
; Sequence 11, Application US/10810262
; Publication No. US20040234505A1
; GENERAL INFORMATION:
; APPLICANT: KINGSMAN, SUSAN MARY
; APPLICANT: BINLEY, KATIE
; TITLE OF INVENTION: POLYNUCLEOTIDE CONSTRUCTS AND USES THEREOF
; FILE REFERENCE: 674523-2029.1
; CURRENT FILING DATE: US/10/810,262
; CURRENT FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: 09/787,562
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: PCT/GB99/03181
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/GB98/02885
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: GB 9901906.9
; PRIOR FILING DATE: 1999-01-28
; PRIOR APPLICATION NUMBER: GB 9903538.8
; PRIOR FILING DATE: 1999-02-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 11
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-810-262-11

Query Match 99.7%; Score 1535; DB 5; Length 303;
Best Local Similarity 99.6%; Pred. No. 7.2e-120;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGYRTGMSKNGITCQKWSSTSPHRPRFSPATHPSGLEENYCRNPDN 60
DB 33 VYLSECKTGNGKNGYRTGMSKNGITCQKWSSTSPHRPRFSPATHPSGLEENYCRNPDN 92

QY 61 DPQGPWCYTTDPKRYDYCDILLECEBECMHCSENYDGKISKTMGLCQAWDSQSPHAH 120
DB 93 DPQGPWCYTTDPKRYDYCDILLECEBECMHCSENYDGKISKTMGLCQAWDSQSPHAH 152

QY 121 GYIPSKFPNKLKKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTTPPSSGPTYQCILK 180
DB 153 GYIPSKFPNKLKKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTTPPSSGPTYQCILK 212

QY 181 GTGENYRGNAVTVSGHTCQHSQAQTPHTHTPTNPENFPCKNLDENYCRNPDGKRAPWCHT 240
DB 213 GTGENYRGNAVTVSGHTCQHSQAQTPHTHTNPENFPCKNLDENYCRNPDGKRAPWCHT 272

QY 241 TNSQVRWEYCKIPSCDSSPV 260
DB 273 TNSQVRWEYCKIPSCDSSPV 292

RESULT 3

US-09-788-142-3
; Sequence 3, Application US/09788142
; Patent No. US20010029246A1
; GENERAL INFORMATION:
; APPLICANT: Folkman, M. Judah
; TITLE OF INVENTION: Angiostatin Fragments and Method of Use
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jones & Askew, LLP
; STREET: 191 Peachtree Street, 37th Floor
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303-1769
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/788,142
FILING DATE: 16-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/866,735
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05940-0129
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 818-3700
TELEFAX: (404) 818-3799
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: Angiostatin fragment
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-788-142-3

Query Match 99.7%; Score 1535; DB 3; Length 339;
Best Local Similarity 99.6%; Pred. No. 8.2e-120;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGYRTGMSKNGITCQKWSSTSPHRPRFSPATHPSGLEENYCRNPDN 60
DB 1 VYLSECKTGNGKNGYRTGMSKNGITCQKWSSTSPHRPRFSPATHPSGLEENYCRNPDN 60

QY 61 DPQGPWCYTTDPKRYDYCDILLECEBECMHCSENYDGKISKTMGLCQAWDSQSPHAH 120
DB 61 DPQGPWCYTTDPKRYDYCDILLECEBECMHCSENYDGKISKTMGLCQAWDSQSPHAH 120

QY 121 GYIPSKFPNKLKKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTTPPSSGPTYQCILK 180
DB 121 GYIPSKFPNKLKKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTTPPSSGPTYQCILK 180

QY 181 GTGENYRGNAVTVSGHTCQHSQAQTPHTHTPTNPENFPCKNLDENYCRNPDGKRAPWCHT 240
DB 181 GTGENYRGNAVTVSGHTCQHSQAQTPHTHTNPENFPCKNLDENYCRNPDGKRAPWCHT 240

QY 241 TNSQVRWEYCKIPSCDSSPV 260
DB 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 4
US-09-761-120-3
; Sequence 3, Application US/09761120
; Patent No. US20020037847A1
; GENERAL INFORMATION:
; APPLICANT: Folkman, M. Judah
; APPLICANT: O'Reilly, Michael
; TITLE OF INVENTION: Nucleic Acids Encoding Kringle 1-5 Region Fragments of Plasminogen
; FILE REFERENCE: 05940-0151 (43171-252068)
; CURRENT APPLICATION NUMBER: US/09/761,120
; CURRENT FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 09/309,821
; PRIOR FILING DATE: 1999-05-11

;; PRIOR APPLICATION NUMBER: 08/866,735
;; PRIOR FILING DATE: 1997-05-30
;; NUMBER OF SEQ ID NOS: 47
;; SOFTWARE: Patent in version 3.0
;; SEQ ID NO 3
;; LENGTH: 339
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-761-120-3

Query Match 99.7%; Score 1535; DB 3; Length 339;
Best Local Similarity 99.6%; Pred. No. 8.2e-120;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 VYLSECKTGNKNGYGTMSKTKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN 60
DB 1 VYLSECKTGNKNGYGTMSKTKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN 60
QY 61 DQGGPWCYTTDPKRYDYCDILECEECHSCGENYDGKISKTMSGLECOAWDSQSPHAA 120
DB 61 DQGGPWCYTTDPKRYDYCDILECEECHSCGENYDGKISKTMSGLECOAWDSQSPHAA 120
QY 121 GYIPSKFPNKNLKNYCRNPDRELAPWCFTTDPNKRWELCDIPRCTTTPPPSSGPTYQCLK 180
DB 121 GYIPSKFPNKNLKNYCRNPDRELAPWCFTTDPNKRWELCDIPRCTTTPPPSSGPTYQCLK 180
QY 181 GTGENYRGNAVTVSGHTCQHSQAOTPHHTERTPTENFPCKNLNDENYCRNPDGKRAPWCHT 240
DB 181 GTGENYRGNAVTVSGHTCQHSQAOTPHHTERTPTENFPCKNLNDENYCRNPDGKRAPWCHT 240
QY 241 TNSQVRWEYCKIPSCDSSPV 260
DB 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 5

US-09-335-325-3
; Sequence 3, Application US/09335325
; Patent No. US20020164717A1

GENERAL INFORMATION:

;; APPLICANT: Folkman, M. Judah
;; O'Reilly, Micheal
;; Cao, Yihai
;; Sim, B. Kim Lee
;; TITLE OF INVENTION: Angiostatin Fragments and Method of Use
;; NUMBER OF SEQUENCES: 45
;; CORRESPONDENCE ADDRESS:
;; ADDRESSER: Jones & Askew
;; STREET: 191 Peachtree Street, 37th Floor
;; CITY: Atlanta
;; STATE: Georgia
;; COUNTRY: U.S.
;; ZIP: 30303-1769
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent in Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/335,325
;; FILING DATE: 17-Jun-1999
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/612,788
;; FILING DATE: <Unknown>
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Warren, William L.
;; REGISTRATION NUMBER: 36,714
;; REFERENCE/DOCKET NUMBER: 05213-0126
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 404-818-3700
;; TELEFAX: 404-818-3799
;; INFORMATION FOR SEQ ID NO: 3:

;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 339 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: <Unknown>
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; FRAGMENT TYPE: N-terminal
;; ORIGINAL SOURCE:
;; ORGANISM: Homo sapiens
;; IMMEDIATE SOURCE:
;; CLONE: Angiostatin fragment
;; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-335-325-3
Query Match 99.7%; Score 1535; DB 3; Length 339;
Best Local Similarity 99.6%; Pred. No. 8.2e-120;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 VYLSECKTGNKNGYGTMSKTKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN 60
DB 1 VYLSECKTGNKNGYGTMSKTKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN 60
QY 61 DQGGPWCYTTDPKRYDYCDILECEECHSCGENYDGKISKTMSGLECOAWDSQSPHAA 120
DB 61 DQGGPWCYTTDPKRYDYCDILECEECHSCGENYDGKISKTMSGLECOAWDSQSPHAA 120
QY 121 GYIPSKFPNKNLKNYCRNPDRELAPWCFTTDPNKRWELCDIPRCTTTPPPSSGPTYQCLK 180
DB 121 GYIPSKFPNKNLKNYCRNPDRELAPWCFTTDPNKRWELCDIPRCTTTPPPSSGPTYQCLK 180
QY 181 GTGENYRGNAVTVSGHTCQHSQAOTPHHTERTPTENFPCKNLNDENYCRNPDGKRAPWCHT 240
DB 181 GTGENYRGNAVTVSGHTCQHSQAOTPHHTERTPTENFPCKNLNDENYCRNPDGKRAPWCHT 240
QY 241 TNSQVRWEYCKIPSCDSSPV 260
DB 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 6

US-10-131-241-3
; Sequence 3, Application US/10131241
; Publication No. US20030012792A1

GENERAL INFORMATION:

;; APPLICANT: Holaday, John W.
;; APPLICANT: Fortier, Anne H.
;; TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Proliferation
;; TITLE OF INVENTION: and Regulating Angiogenesis Using Cancer Markers
;; FILE REFERENCE: 05213-0344 43170-271565
;; CURRENT APPLICATION NUMBER: US/10/131,241
;; CURRENT FILING DATE: 2002-07-22
;; PRIOR APPLICATION NUMBER: US 09/413,049
;; PRIOR FILING DATE: 1999-10-06
;; PRIOR APPLICATION NUMBER: US 09/316,802
;; PRIOR FILING DATE: 1999-05-21
;; PRIOR APPLICATION NUMBER: US 60/086,586
;; PRIOR FILING DATE: 1998-05-22
;; NUMBER OF SEQ ID NOS: 65
;; SOFTWARE: Patent in version 3.1
;; SEQ ID NO 3
;; LENGTH: 339
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-131-241-3
Query Match 99.7%; Score 1535; DB 4; Length 339;
Best Local Similarity 99.6%; Pred. No. 8.2e-120;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 VYLSECKTGNKNGYGTMSKTKNGITCQKWSSTSPHRPSPATHPSEGLEENYCRNPDN 60

Db 1 VYLSECKTGNGKNGYRTGMSKTKNGITCQKWSSTSPHRPRFSPATHPSGLEENYCRNPDN 60
QY 61 DQGGPWCYTTDPKRYDYCDILECEECMHCSENGYDGIKSKTMSGLECQAWDSOSPHAH 120
Db 61 DQGGPWCYTTDPKRYDYCDILECEECMHCSENGYDGIKSKTMSGLECQAWDSOSPHAH 120
QY 121 GYIPSKFPNKLKKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTTPPPSSGPTYQCLK 180
Db 121 GYIPSKFPNKLKKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTTPPPSSGPTYQCLK 180
QY 181 GTGENYRGNVAVTVSGHTCOHWSAQTPHTHTERTPENFPCKNLNDENYCRNPDGKRAPWCHT 240
Db 181 GTGENYRGNVAVTVSGHTCOHWSAQTPHTHTERTPENFPCKNLNDENYCRNPDGKRAPWCHT 240
QY 241 TNSQVRWEYCKIPSCDSSPV 260
Db 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 7

US-10-127-066-3
; Sequence 3, Application US/10127066
; Publication No. US20030064926A1
; GENERAL INFORMATION:
; APPLICANT: O'Reilly, Michael S.
; APPLICANT: Folkman, M. Judah
; APPLICANT: Cao, Yihai
; APPLICANT: Sim, Kim Lee
; TITLE OF INVENTION: Angiostatin Fragments and Method of Use
; FILE REFERENCE: 05213-0612 43170-272529
; CURRENT APPLICATION NUMBER: US/10/127,066
; CURRENT FILING DATE: 2002-07-23
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 3
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-127-066-3

Query Match 99.7%; Score 1535; DB 4; Length 339;
Best Local Similarity 99.6%; Pred. No. 8.2e-120;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGYRTGMSKTKNGITCQKWSSTSPHRPRFSPATHPSGLEENYCRNPDN 60
Db 1 VYLSECKTGNGKNGYRTGMSKTKNGITCQKWSSTSPHRPRFSPATHPSGLEENYCRNPDN 60
QY 61 DQGGPWCYTTDPKRYDYCDILECEECMHCSENGYDGIKSKTMSGLECQAWDSOSPHAH 120
Db 61 DQGGPWCYTTDPKRYDYCDILECEECMHCSENGYDGIKSKTMSGLECQAWDSOSPHAH 120
QY 121 GYIPSKFPNKLKKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTTPPPSSGPTYQCLK 180
Db 121 GYIPSKFPNKLKKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTTPPPSSGPTYQCLK 180
QY 181 GTGENYRGNVAVTVSGHTCOHWSAQTPHTHTERTPENFPCKNLNDENYCRNPDGKRAPWCHT 240
Db 181 GTGENYRGNVAVTVSGHTCOHWSAQTPHTHTERTPENFPCKNLNDENYCRNPDGKRAPWCHT 240
QY 241 TNSQVRWEYCKIPSCDSSPV 260
Db 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 8

US-10-402-364-3
; Sequence 3, Application US/10402364
; Publication No. US20040002459A1
; GENERAL INFORMATION:
; APPLICANT: O'Reilly, Michael
; APPLICANT: Folkman, M. Judah
; TITLE OF INVENTION: Nucleic Acids Encoding Kringle 1-5 Region Fragments of Plasminogen

; FILE REFERENCE: 05213-2151 (43170-252068)
; CURRENT APPLICATION NUMBER: US/10/402,364
; CURRENT FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: US/09/761,120A
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 09/309,821
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 08/866,735
; PRIOR FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 3
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-402-364-3

Query Match 99.7%; Score 1535; DB 4; Length 339;
Best Local Similarity 99.6%; Pred. No. 8.2e-120;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGYRTGMSKTKNGITCQKWSSTSPHRPRFSPATHPSGLEENYCRNPDN 60
Db 1 VYLSECKTGNGKNGYRTGMSKTKNGITCQKWSSTSPHRPRFSPATHPSGLEENYCRNPDN 60
QY 61 DQGGPWCYTTDPKRYDYCDILECEECMHCSENGYDGIKSKTMSGLECQAWDSOSPHAH 120
Db 61 DQGGPWCYTTDPKRYDYCDILECEECMHCSENGYDGIKSKTMSGLECQAWDSOSPHAH 120
QY 121 GYIPSKFPNKLKKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTTPPPSSGPTYQCLK 180
Db 121 GYIPSKFPNKLKKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTTPPPSSGPTYQCLK 180
QY 181 GTGENYRGNVAVTVSGHTCOHWSAQTPHTHTERTPENFPCKNLNDENYCRNPDGKRAPWCHT 240
Db 181 GTGENYRGNVAVTVSGHTCOHWSAQTPHTHTERTPENFPCKNLNDENYCRNPDGKRAPWCHT 240
QY 241 TNSQVRWEYCKIPSCDSSPV 260
Db 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 9

US-10-401-108-3
; Sequence 3, Application US/10401108
; Publication No. US20040023877A1
; GENERAL INFORMATION:
; APPLICANT: Folkman, M. Judah
; APPLICANT: O'Reilly, Michael
; TITLE OF INVENTION: Angiostatin Fragments and Method of Use
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jones & Askew, LLP
; STREET: 191 Peachtree Street, 37th Floor
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303-1769
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/401,108
; FILING DATE: 27-Mar-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/866,735
; FILING DATE: 30-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren, William L.
; REGISTRATION NUMBER: 36,714

REFERENCE/DOCKET NUMBER: 05940-0129
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 818-3700
TELEFAX: (404) 818-3799
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: Angiostatin fragment
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-401-108-3

Query Match 99.7%; Score 1535; DB 4; Length 339;
Best Local Similarity 99.6%; Pred. No. 8.2e-120;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSEKKTGKNGYRTGKNGITCQKWSSTSPHRPSPATHSEGLEENYCRNPDN 60
DB 1 VYLSEKKTGKNGYRTGKNGITCQKWSSTSPHRPSPATHSEGLEENYCRNPDN 60
QY 61 DPOGWCYTTDPKRYDYCDILECEBECMHCSENGYDGKISKTMGLSCQAWDSQSPH 120
DB 61 DPOGWCYTTDPKRYDYCDILECEBECMHCSENGYDGKISKTMGLSCQAWDSQSPH 120
QY 121 GYIPSKFPNNLKNKYNCRNPDRELRCWELCDIPRCTTTPPSSGPTYQCLK 180
DB 121 GYIPSKFPNNLKNKYNCRNPDRELRCWELCDIPRCTTTPPSSGPTYQCLK 180
QY 181 GTGENTRGNAVTVSGHTCOHWSAQTPHTHRTPENPPCKNLNLDENYCRNPDGKRAPWCHT 240
DB 181 GTGENTRGNAVTVSGHTCOHWSAQTPHTHRTPENPPCKNLNLDENYCRNPDGKRAPWCHT 240
QY 241 TNSQVRWEYCKIPSCDSSPV 260
DB 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 10
US-11-010-874-3
; Sequence 3, Application US/11010874
; Publication No. US20050250694A1
; GENERAL INFORMATION:
; APPLICANT: Ma, Jian-King
; TITLE OF INVENTION: COMPOUNDS USEFUL IN INHIBITING VASCULAR LEAKAGE, INFLAMMATION AND
; TITLE OF INVENTION: FIBROSIS AND METHODS OF MAKING AND USING SAME
; FILE REFERENCE: 5820.656
; CURRENT APPLICATION NUMBER: US/11/010,874
; PRIOR FILING DATE: 2004-12-13
; PRIOR FILING DATE: 10/963,115
; PRIOR FILING DATE: 2004-10-12
; PRIOR FILING DATE: 60/510,620
; PRIOR FILING DATE: 2003-10-10
; PRIOR FILING DATE: 60/528,647
; PRIOR FILING DATE: 2003-12-11
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-010-874-3

Query Match 99.7%; Score 1535; DB 6; Length 339;
Best Local Similarity 99.6%; Pred. No. 8.2e-120;

Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSEKKTGKNGYRTGKNGITCQKWSSTSPHRPSPATHSEGLEENYCRNPDN 60
DB 1 VYLSEKKTGKNGYRTGKNGITCQKWSSTSPHRPSPATHSEGLEENYCRNPDN 60
QY 61 DPOGWCYTTDPKRYDYCDILECEBECMHCSENGYDGKISKTMGLSCQAWDSQSPH 120
DB 61 DPOGWCYTTDPKRYDYCDILECEBECMHCSENGYDGKISKTMGLSCQAWDSQSPH 120
QY 121 GYIPSKFPNNLKNKYNCRNPDRELRCWELCDIPRCTTTPPSSGPTYQCLK 180
DB 121 GYIPSKFPNNLKNKYNCRNPDRELRCWELCDIPRCTTTPPSSGPTYQCLK 180
QY 181 GTGENTRGNAVTVSGHTCOHWSAQTPHTHRTPENPPCKNLNLDENYCRNPDGKRAPWCHT 240
DB 181 GTGENTRGNAVTVSGHTCOHWSAQTPHTHRTPENPPCKNLNLDENYCRNPDGKRAPWCHT 240
QY 241 TNSQVRWEYCKIPSCDSSPV 260
DB 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 11
US-10-292-418-11
; Sequence 11, Application US/10292418
; Publication No. US20030139365A1
; GENERAL INFORMATION:
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Li, Yue
; APPLICANT: Gillies, Stephen D
; TITLE OF INVENTION: Expression and Export of Angiogenesis Inhibitors as
; TITLE OF INVENTION: Immunofusins
; FILE REFERENCE: LEX-006C1
; CURRENT APPLICATION NUMBER: US/10/292,418
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: 09/383,315
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: US 60/097,883
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-418-11

Query Match 99.7%; Score 1535; DB 4; Length 363;
Best Local Similarity 99.6%; Pred. No. 8.9e-120;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSEKKTGKNGYRTGKNGITCQKWSSTSPHRPSPATHSEGLEENYCRNPDN 60
DB 2 VYLSEKKTGKNGYRTGKNGITCQKWSSTSPHRPSPATHSEGLEENYCRNPDN 61
QY 61 DPOGWCYTTDPKRYDYCDILECEBECMHCSENGYDGKISKTMGLSCQAWDSQSPH 120
DB 62 DPOGWCYTTDPKRYDYCDILECEBECMHCSENGYDGKISKTMGLSCQAWDSQSPH 121
QY 121 GYIPSKFPNNLKNKYNCRNPDRELRCWELCDIPRCTTTPPSSGPTYQCLK 180
DB 122 GYIPSKFPNNLKNKYNCRNPDRELRCWELCDIPRCTTTPPSSGPTYQCLK 181
QY 181 GTGENTRGNAVTVSGHTCOHWSAQTPHTHRTPENPPCKNLNLDENYCRNPDGKRAPWCHT 240
DB 182 GTGENTRGNAVTVSGHTCOHWSAQTPHTHRTPENPPCKNLNLDENYCRNPDGKRAPWCHT 241
QY 241 TNSQVRWEYCKIPSCDSSPV 260
DB 242 TNSQVRWEYCKIPSCDSSPV 261

RESULT 12

US-09-873-676-1
; Sequence 1, Application US/09873676
; Patent No. US20020077289A1
; GENERAL INFORMATION:
; APPLICANT: Macdonald, Nicholas J.
; APPLICANT: Sim, Kim L.
; TITLE OF INVENTION: Angiostatin and Endostatin Binding Proteins and Methods of Use
; FILE REFERENCE: 05213-0378 (43170-259333)
; CURRENT APPLICATION NUMBER: US/09/873,676
; CURRENT FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: US 60/209,065
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: US 60/289,387
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-873-676-1

Query Match 99.7%; Score 1535; DB 3; Length 378;
Best Local Similarity 99.6%; Pred. No. 9.3e-120;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGYGTGWSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN 60
DB 6 VYLSECKTGNGKNGYGTGWSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN 65

QY 61 DQGGPWCYTTDPEKRYDYCDILECEECHMCSGENYDGIKSKTMSGLECOAWDSQSPHAH 120
DB 66 DQGGPWCYTTDPEKRYDYCDILECEECHMCSGENYDGIKSKTMSGLECOAWDSQSPHAH 125

QY 121 GYIPSKFPNKLKKNYCRNPDRELPCWCTTDPNKRWELCDIPRCTTPPPSSGPTYQCLK 180
DB 126 GYIPSKFPNKLKKNYCRNPDRELPCWCTTDPNKRWELCDIPRCTTPPPSSGPTYQCLK 185

QY 181 GTGENYRGNAVTVSGHTCQHSQAQTPHTHTPTENFPCKNLNDENYCRNPDGKRAPWCHT 240
DB 186 GTGENYRGNAVTVSGHTCQHSQAQTPHTHTPTENFPCKNLNDENYCRNPDGKRAPWCHT 245

QY 241 TNSQVRWEYCKIPSCDSSPV 260
DB 246 TNSQVRWEYCKIPSCDSSPV 265

RESULT 13

US-09-335-325-42
; Sequence 42, Application US/09335325
; Patent No. US20020164717A1
; GENERAL INFORMATION:
; APPLICANT: Folkman, M. Judah
; Cao, Yihai
; Sim, B. Kim Lee

TITLE OF INVENTION: Angiostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSER: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/335,325

FILING DATE: 17-Jun-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/612,788
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05213-0126
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: K1-4BKLS
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-09-335-325-42

Query Match 99.7%; Score 1535; DB 3; Length 378;
Best Local Similarity 99.6%; Pred. No. 9.3e-120;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGYGTGWSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN 60
DB 6 VYLSECKTGNGKNGYGTGWSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN 65

QY 61 DQGGPWCYTTDPEKRYDYCDILECEECHMCSGENYDGIKSKTMSGLECOAWDSQSPHAH 120
DB 66 DQGGPWCYTTDPEKRYDYCDILECEECHMCSGENYDGIKSKTMSGLECOAWDSQSPHAH 125

QY 121 GYIPSKFPNKLKKNYCRNPDRELPCWCTTDPNKRWELCDIPRCTTPPPSSGPTYQCLK 180
DB 126 GYIPSKFPNKLKKNYCRNPDRELPCWCTTDPNKRWELCDIPRCTTPPPSSGPTYQCLK 185

QY 181 GTGENYRGNAVTVSGHTCQHSQAQTPHTHTPTENFPCKNLNDENYCRNPDGKRAPWCHT 240
DB 186 GTGENYRGNAVTVSGHTCQHSQAQTPHTHTPTENFPCKNLNDENYCRNPDGKRAPWCHT 245

QY 241 TNSQVRWEYCKIPSCDSSPV 260
DB 246 TNSQVRWEYCKIPSCDSSPV 265

RESULT 14

US-10-131-241-42
; Sequence 42, Application US/10131241
; Publication No. US20030012792A1
; GENERAL INFORMATION:
; APPLICANT: Holaday, John W.
; APPLICANT: Fortier, Anne H.
; TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Proliferation
; TITLE OF INVENTION: and Regulating Angiogenesis Using Cancer Markers
; FILE REFERENCE: 05213-0344 43170-271565
; CURRENT APPLICATION NUMBER: US/10/131,241
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US 09/413,049
; PRIOR FILING DATE: 1999-10-06
; PRIOR APPLICATION NUMBER: US 09/316,802
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: US 60/086,586
; PRIOR FILING DATE: 1998-05-22
; NUMBER OF SEQ ID NOS: 65

Search completed: August 29, 2006, 14:16:57
Job time : 182 secs

Query Match	99.7%	Score 1535;	DB 4;	Length 378;
Best Local Similarity	99.6%	Pred. No. 9.3e-120;		
Matches 259; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

Qy	1	VYLSECKTGNKNGYGTMTSKTNGITCQKWSSTSPHPRPSPATHPSGLEGLEENYCRNP	60
Db	6	VYLSECKTGNKNGYGTMTSKTNGITCQKWSSTSPHPRPSPATHPSGLEGLEENYCRNP	65
Qy	61	DPOGPWCYTTPDPEKRYDYCDILECEEBCMHCSGENYDGKISKTMGSLGECQAWDSQSPH	120
Db	66	DPOGPWCYTTPDPEKRYDYCDILECEEBCMHCSGENYDGKISKTMGSLGECQAWDSQSPH	125
Qy	121	GYTPSKPPNKLKNYCRNPDRRLRPMCFTTDPNKRWELCDIPRCTTTPPSSGPTYOCLK	180
Db	126	GYTPSKPPNKLKNYCRNPDRRLRPMCFTTDPNKRWELCDIPRCTTTPPSSGPTYOCLK	185
Qy	181	GTGENYRGNAVTVSGHTCOHWSAQTPHTHTERTPENPCKNLDENYCRNPDGKRAPWCHT	240
Db	186	GTGENYRGNAVTVSGHTCOHWSAQTPHTHTERTPENPCKNLDENYCRNPDGKRAPWCHT	245
Qy	241	TNSQVRWEYCKIPSCDSSPV	260
Db	246	TNSQVRWEYCKIPSCDSSPV	265

RESULT 15

```

US-10-127-066-42
; Sequence 42, Application US/10127066
; Publication No. US20030064926A1
; GENERAL INFORMATION:
; APPLICANT: O'Reilly, Michael S.
; APPLICANT: Polkman, M. Judah
; APPLICANT: Cao, Yihai
; APPLICANT: Sim, Kim Lee
; TITLE OF INVENTION: Angiostatin Fragments and Method of Use
; FILE REFERENCES: 05213-0612 43170-272529
; CURRENT APPLICATION NUMBER: US/10/127,066
; CURRENT FILING DATE: 2002-07-23
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-127-066-42

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Query Match      99.7%; Score 1535; DB 4; Length 378;
Best Local Similarity 99.6%; Pred. No. 9.3e-120;
Matches 259: Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy	1	VYLSECKTGKNGKNGTMSKTKNGITCQKWSSTSPHPRPSPATHPSEGLEENYCRNPDN	60
Db	6	VYLSECKTGKNGKNGTMSKTKNGITCQKWSSTSPHPRPSPATHPSEGLEENYCRNPDN	65
Qy	61	DPOGPWCYTTDPKRYDYCDILECEERCMHCSGENYDGKISKTMGILECQAWDSQSPHAF	120
Db	66	DPOGPWCYTTDPKRYDYCDILECEERCMHCSGENYDGKISKTMGILECQAWDSQSPHAF	125
Qy	121	GYTPSKPKNLKNKYNCRNPDRRLRPMCFTTDPNKRWELCDIPRCTTTPPSSSGPTYCCLK	180
Db	126	GYTPSKPKNLKNKYNCRNPDRRLRPMCFTTDPNKRWELCDIPRCTTTPPSSSGPTYCCLK	185
Qy	181	GTGENYRGNAVTVVSIGHTCQHSQAOTPHTHERTPENFPCKNLDSNYCRNPDGKRAPMCHT	240
Db	186	GTGENYRGNAVTVVSIGHTCQHSQAOTPHTHERTPENFPCKNLDSNYCRNPDGKRAPMCHT	245

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